

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCTAGAGATCCCTCGACCTCGA
CCCACGCGTCCGGGCCGGAGCAGCACGGCCGAGGACCTGGAGCTCCGGCTCGCTCTCCCG
CAGCGCTACCCGCCATGCGCCTGCCGCGCGGGCCGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCGCGGAGGCCGCCAAGAAGCCGACGCCCTGCCACCGGTGCCGGGGGT
GGTGGACAAGTTTAAACCAGGGGATGGTGGACACCGCAAAGAAGAACTTTGGCGCGGGAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTTCGCTCTGGAGATC
CTGGAGGGGCTGTGCGAGAGCAGCGACTTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCTGTGTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTTCGAGTGGTTT
GTGTGAAGACTGAAAGTGTGTCTCTCCAGGAACCTACGGTCCCGACTGTCTCGCATGC
CAGGGCGGATCCAGAGGCCCTGCAGCGGGAATGGCCACTGCAGCGGAGATGGGAGCAGACA
GGGCGACGGGTCTGCCGTGCCACATGGGGTACCAGGGCCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGTCTCGGGCTGACCAACAGAGACTCGGCGAGTGTGAAGTGGGTGGGTGT
GGACGAGGGCGCTGTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTGTG
GGCTGCACAGGGGAAGGCCAGGAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAGATGTGGACGAGTGTCTACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAACTGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCTCTGACGGCTTCGAAGAAACG
GAAGATGCCTGTGTGCCGCCGGCAGAGGCTGAAGCCACAGAAGGAGAAAAGCCCGACACAGCT
GCCCTCCCGCAAGACCTGTAAAGTGTGCCGACTTACCCTTTAAATTATTTCAGAAGGATGTCC
CGTGGAAAATGTGGCCCTGAGGATGCCGTCTCTGCAGTGGACAGCGCGGGGAGAGGCTGC
CTGCTCTCTAACCGTTGATTCTCATTTGTCCCTTAAACAGCTGCATTTCTTGGTTGTTCTTA
AACAGACTGTATATTTTGATACAGTTCTTTGTAATAAAATGACCATTTGTAGGTAATCAGG
AGGAAAAAAAAAAAAAAAAAAAAAAAAAGGGCGGCGGACTCTAGAGTCGACCTGCAGAAGC
TTGGCCGGCATGGCCAACTGTATTATGCAGCTTATAATGTTACAAATAAAGCAATAGCA
TCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGGAATTAATTCGGCGCAGCACCATTGGCCTGAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGGAAAGAACAGCTGTGGAATG
TGTGTCAATTAGGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTTT

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FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop
><MW: 38192, pI: 4.53, NX(S/T): 2
MRLPRRAALGLLPLLLLLPPAPEAAKKPTPCHRCRGLVDKFNQGMVD TAKKNFGGGNTAWEETLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFVCVKT LKVCSPGTYPGDC LACQGGSGRQPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNETHS ICTACDESKTCSGLTNRDCGECEVGWVLDE
GACVDVDECAAEPFPCSAQAQCKNANGSYTCEECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDECSLAEKT
CVRKNENCYNTPGSYVCVCPDGFEEETEDACVPPAEAEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

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FIGURE 3

CAGGTCCTCACTGCACCTCGGTTCTATCGATTGAATTCCTCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGCTCCGCCAGGCCGGGAGGCGACGCGCCAGCCGCTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGGCGAGCGAGGAGGTCCTGAGCAGCATGGCCCGGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCCTGTGCCCTGCTGGCACTGGGGGCGGAGGC
CGGGCGCGCGCAGGAGGAGAGCCTGTACCTATGGATCGATGCTCACAGGCAAGAGTACTCA
TAGGATTTGAAGAAGATATCCTGATTGTTTCAGAGGGGAAATGGCACCTTTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTTAC
CTGGCAAGCTGCGAGGCGAGGCAAACTACTTCTATGAATTCCTGTCTCTCGCTCCCTGGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGGAACAGTGCCCTCACAAAGCA
TCAGTTGTTCAAGTTGGTTTCCCATGTCTTGGAAAAACAGGATGGGGTGGCAGCATTGGAAGT
GGATGTGATTGTTATGAATTCCTGAAGGCAACACCATTCTCCAAACACCTCAAATGCTATCT
TCTTTAAACATGTCAACAAGCTGAGTGCCCGAGCGGGTGCCGAAATGGAGGCTTTTGTAAAT
GAAAGACGCATCTGCGAGTGTCTGATGGGTTCCACGGACCTCACTGTGAGAAAAGCCCTTG
TACCCACGATGTATGAATGGTGGACTTTGTGTGACTCCTGGTTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAGTGTGACAAAGCAAAGTCTCAACCACCTGCTTTAATGGAGGGACC
TGTTTCTACCTTGGAAAAATGTATTGCCCCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAAATGCCCAACAACCTGTGCAAAATGGAGGTAATGTCATTGGTAAAGCAAAATGTAAAGTGT
CCAAAGGTTTACCAGGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTGACAT
GGAACCTGCCATGAACCCAAACAAATGCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGGCGCCGAGCTCAGGCAGC
ACACGCCCTTCACTTAAAAAGGCCGAGGAGCGGCGGGATCCACCTGAATCCAATTACATCTGG
CGAACTCCGACATCTGAAACGTTTAAAGTTACACCAAGTTTCATAGCCTTTGTTAACTTTTCA
TGTGTTGAATGTTCAAATAATGTTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAATCACTGAGCTGATATTTACTCTTCTTTTAAAGTTTCTAAGTACGCTCTGTAG
CATGATGGTATAGATTTTCTGTTTTCAGTGCTTTGGGACAGATTTTATATTATGTCAATTGA
TCAGGTTAAAAATTTTCAGTGTGTAGTTGGCAGATATTTCAAATTAACAATGCATTTATGGT
GTCTGGGGGCGAGGGGAACATCAGAAAGGTTAAATTTGGGCAAAATGCGTAAAGTCAACAAGAA
TTGGATGGTGCACTTAATGTTGAAGTTACAGCATTTCAGATTTTATTGTGAGATTTTATAGAT
GTTTGTACATTTTAAAAAATGCTCTTAATTTTAACTCTCAATACAATATATTTTGACC
TTACCATTATTCAGAGATTTCAGTATTAATAAAAAAAAAAATTAACCTGTGGTAGTGGCATTT
AAACAATATAATATATTTCAAACAATGAATAGGGAATATAATGTATGAACCTTTTTCAT
TGGCTTGAAGCAATATAATATATGTAAACAAAACACAGCTCTTACCTAATAAACATTTTAT
ACTGTTTGTATGTATAAAAAATAAGGTGCTGCTTTAGTTTTTGGAAAAAATAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAGGCGCGCGCACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCACTTGTTTATTGCAGCTTATAATG

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FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLSILLCLLALRAEAGPPQEESELYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAIFYEFLSLRLDKGIMADPTVNVPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPHEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCICPPGLEGEQCEISKCPQPCRNGGKCIGKSKCKSKGYQGDLCSPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERDRP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

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FIGURE 5

CGGACGCGTGGGCGTCCGCGGTCGCAGAGCCAGGAGGCGGAGGCGCGCGGGCCAGCCTGGG
CCCCAGCCCCACACCTTCACCAGGGCCAGGAGCCACCATGTGGCGATGTCCACTGGGGCTAC
TGCTTTGTCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCTGTGGGCGCCGG
GAGCTAGCACCCGGGTCTGCACCTGCGGGGCATCCGGGACGCGGGAGGCCGCTACTGCCAGGA
GCAGGACCTGTGCTGCCGCGGGCGGTGCCGACGACTGTGCCCTGCCCTACTCTGGGCGGCATCT
GTTACTGTGACCTCTTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTTTCCCGCATCCAAGGATGTATGCATGGAGGTCTGATCTA
TCCAGTCTTGGGAACTGATGGGCAACTGTAAACGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTTCTGGGGCATGACCTGGATGAGGGCATTCGCTACCGCTGGGCACCA
TCCGCCCATCTTCTCGGTATGAACATGCATGAAATTTATACAGTGTGAACCCAGGGGAG
GTGCTTCCACAGCCCTTCGAGGCTCTGAGAAGTGGCCCACTGATTATGAGCCTCTTGA
CCAAGGCAACTGTGAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATCTCTGGGACACATGACGCTGTCTGTGCGCCCAAGAACCTGTCTGTCTGTGAC
ACCCACAGCAGCAGGGCTGCCGCGGTGGGCGTCTCGATGGTGCCTGGTGGTTCCTGCGTGC
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTTCTCGGGCGGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCC
CACTGCCCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGC
CTTGGAGGCCAGAGAGATACCGCGGCATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCGGCCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGGCCACTTCCGCATCGTGC CGGCGCTCAATGAGTGCAGACATCGAG
AGCTTCTGTCTGGGCTCTGGGGCGCGTGGGCATGGAGACATGGGTCTCATCTGAGGCTG
CGGGCACCACGCGGGTCCGGCTGGGATCCAGGCTAAGGGCCGCGGGAAGAGGCCCAATG
GGCGGTGACCCGCTCGCCCGACAGAGCCCGGGCGCAGGCGGGCGCCAGGGCGCTAAT
CCCGGCGCGGGTTCGCTGACGCGAGCGCCCGCTGGGAGCGCGGGCAGGCAGACTGGCG
GAGCCCCAGACCTCCAGTGGGGACGGGGCAGGCGCTGGCCTGGGAAGAGCACAGCTGCAG
ATCCAGGCGCTGCGCGCCCCACTCAAGACTACCAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCCGTATTCTTTTTTTTTTTTTTTTATAGACAGGGTCTTGCTCCG
TTGCCAGGTGGAGTGCAGTGGCCATCAGGGCTCACTGTAACTCCGACTCCTGGGTTCA
AGTGACCTCCCACTCAGCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACACTGGC
TAATTTTTGTATTTTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTTCAACT
CCTGGGCTCAAGCGGTCCACTGCCTCCGCTCCCAAAGTGTGGGATTGCAGGCATGAGCC
ACTGCACCCAGCCTGTATTCTTATTCTCAGATATTTATTTTTCTTTTCACTGTTTTAAAA
TAAACCAAGATTGATAAAAAAAA

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FIGURE 6

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223

><subunit 1 of 1, 164 aa, 1 stop

><MW: 18359, pI: 7.45, NX(S/T): 1

MWRCPLGLLLLLPLAGHLALGAQQGRRRELAPGLHLRGIRDAGGRYCQEQLCCRGRADD
CALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPFPFPIQGCMHGGRIYPVLGTYWDCNR
CTCQENRQWHGGSRRHDQSHQPGQLWLAGWEPQRLLGHDPG

N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

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FIGURE 7

AGGCTCCTTGGCCCTTTTTCACAGCAAGCTTNTGCNATCCCGATTTCGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCCTGTCCTTTNGCCCCAGAACTGCTGTCTTGTACACCCAC
CAGCAGCAGGGCTGCCGCGNTGGGCGTCTCGATGGTGCCTGGTGGTTCTCGCTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTTCTCGGGCCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGGTGCGGGCAAGCGCCAGGCCACTGCCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCCTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCATGGAGG
TGCATGAGGACTTCTTCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATACCGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCACTGCCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAAC TGCGTGG ATGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCCATGCCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCACACTGGGTGTGGTGCCCCAGGCCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCTGGTTCTCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCCATGGCCCTCTCCAGGACTCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGTCTGCTGTTTC
CATGGCCAGCATTCTCCACCCCTTAACCCCTGTGCTCAGGCACCTCTTCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCTCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGT TAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGGAGTCTCCAGAGATGGGGCCTGGAGGCCTGGAGGAA
GGGGCCAGGCCTCACATTCTGTGGGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

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FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGFMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMVYVCTPVPHDPFPMALSRTPTRQISSSDT
DPPADGPSNPLCCCFHGPFAFSTLNPVLRHLFPQEAFPAHPIYDLSQVNSVVSPPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

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FIGURE 10

CCCACGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACTCAGTACGTGAGGGACCAGGGCGCCATGACC
GACCAGCTGAGCAGGCGGCAGATCCGCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTGCAGGTACCCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTTGCCAAGC
TCATAGTGGAGACGGACACGTTTGGCAGCCGGGTTTCGCATCAAAGGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGGCAAGCTCATCGGAAGCCAGCGGGAGAGCAAAGACTG
CGTGTTCACGGAGATCTGTCTGGAGAACAACATATACGGCCTTCCAGAACGCCCGGCACGAGG
GCTGTTTCATGGCCTTCACGCGGCAGGGGCGGCCCGCCAGGCTTCCCGCAGCCGCCAGAAC
CAGCGCAGGCCCCTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTTCCCCAACCCACGC
CGAGAAGCAGAAGCAGTTCGAGTTTGTGGGCTCCGCCCCACCGCCGGACCAAGCGCACAC
GGCGGCCCCAGCCCCCTCACGTAGTCTGGGAGGCAGGGGCGAGCAGCCCCTGGGCCGCCTCCC
CACCCCTTTCCCTTCTTAATCCAAGGACTGGGCTGGGGTGGCGGGAGGGGAGCCAGATCCCC
GAGGGAGGACCCTGAGGGCCGCGAAGCATCCGAGCCCCCAGCTGGGAAGGGGCAGGCCGGTG
CCCCAGGGGCGGCTGGCACAGTGTCCCCCTTCCCGGACGGGTGGCAGGCCCTGGAGAGGAACT
GAGTGTCAACCCTGATCTCAGGCCACCAGCCTCTGCCGGCCTCCAGCCGGGCTCCTGAAGCC
CGCTGAAAGGTACAGCGACTGAAGCCTTGCGAGACAACCGTCTGGAGGTGGCTGTCTCAAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCCAGCCCCCAAACCTCCTCTGGCTAGACTGTA
GGAAGGGACTTTTGTGTTGTTGTTGTTTTCAGGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCTCACATTCACGACCCAGGCTGCACCCACCCCCAACTCCACGCCC
CGGAATAAAACCATTTTCTCTGC

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FIGURE 11

MGAARLLPNLTLCQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRISATAEDGNKFALKLIVETDTFGSRVRIKGAESEKYICMNRGKLGKPSGKSKDCVFTIVLENNYTAFQONARHEGWFMATFTRQGRPRQASRSRQNRQREAHFIKRLYQGQLPFPNHAEKQKQFEFVGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

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FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTTCTCCCTGTTGAATTTTTTGCACATGGAG
 GACAGCAGCAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGGAGATTATTTTAC
 CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCATCCAGT
 CATTTTGATTTTGCTGTTTATTTTTTTTCTTTTTCTTTTCCACCATGTTGTATTTTAT
 TTCCGTACTTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGGCTTTTTCCT
 GAAGTCTTGGCTTATCATTTCCTGGGGCTCTACTCACAGGTGTCCAAACTCCTGGCCTGCC
 CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGGAAGCTTGACCTCAGTG
 CCTCTTGGGATCCCGAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAATAATGC
 TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGTCTACCTGTATGGCAACC
 AACTGGACGAATTTCCCATGAACCTTCCCAAGAATGTACAGATTCTCCATTTGCAGGAAAAC
 AATATTACAGACCATTTACGGGCTGCTCTTGGCCAGCTCTTGAAGCTTGAAGAGCTGCACCT
 GGATGACAACCTCCATATCCACAGTGGGGGTGGAAGACGGGGCTTCCGGGAGCTATTAGCC
 TCAAAATTGTTGTTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGTTGGGCTTCTGTGGAC
 TTGCAAGAGCTGAGAGTGGATGAAAAATCGAATTGCTGTATATCCGACATGGCCCTCCAGAA
 TCTCACGAGCTTGCGAGCGTCTTATTGTGGACGGGAACCTCCTGACCAACAAGGGTATTCGCCG
 AGGGCACCTTGAGCCATCTCACCAAGCTCAAGGAATTTTCAATTGTACGTAATTCGTTGTCCTC
 CACCCCTCTCCCGATCTCCACAGTAGCCTATCTGATCAGGCTCTATTGTCAGGACAACACGAT
 AAACCACTTCTTTGACAGCCTTCTCAAATCTGCGTAAGCTGGAACGGCTGGATATATCCA
 ACAACCAACTGCGGATGCTGACTCAAGGGGTTTTTGATAATCTCTCCAACCTGAAGCAGCTC
 ACTGCTCGGAATAACCTTGGTTTTGTGACTGCAGTATTAATGGGTACAGAAATGGCTCAA
 ATATATCCCTTCATCTCTCAACGTGCGGGGTTTCATGTGCCAAGTCTCGAACAAGTCCGGG
 GGATGGCCGTGAGGGAATTAATATGAATCTTTTGCTGTGCCACACGACCCCGGCCTG
 CCTCTCTTCAACCCAGCCCAAGTACAGCTTCTCCGACCACTCAGCCTCCACCCCTCTCTAT
 TCCAAACCTAGCAGAAGCTACACGCCCTCCAACCTTACCACATCGAAACTTCCACGATTCT
 CTGACTGGGATGGCAGAGAAAGAGTGACCCACCTATTCTTGAACGGATCCAGCTCTCTATC
 CATTTTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTCTTCCACGTGATGGCATA
 CAAACTCACATGGGTGAAAAATGGGCCACAGTTTAGTAGGGGGCATCGTTACAGGAGCGCATAG
 TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCGATCCACCTATCGGATT
 TGTTTAGTGCCACTGGATGCTTTTAACTACCGCGCGGTAGAAGACACATTGTTTCAGAGGC
 CACCACCCATGCCTCTTATCTGAACAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
 CGTCCCAACAGCATGGGCTCCCCCTTCTGCTGGCGGGCTTGATCGGGGGCGCGGTGATATTT
 GTGCTGGTGGTCTTGCTCAGCGTCTTTTGCTGGCATAATGCACAAAAAGGGGCGTACACCTC
 CCAGAAGTGGAAATACAACCGGGGCGGGCGGAAAGATGATTATTGGGAGGCAGGCACCAAGA
 AGGACAACCTCCATCCTGGAGATGACAGAAACAGTTTTTCAGATCGTCTCCTTAATAACGAT
 CAACTCCTTAAAGGAGATTTACAGACTGCAGCCATTACACCCAAATGGGGCGATTAAATTA
 CACAGACTGCCATATCCCAACAACATGCGATACTGCAACAGCAGCGTGCCAGACCTGGAGC
 ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGCGGACCAATTAGACTCTTGAGAA
 CACACTCGTGTGTGCACATAAAGACACGCAGATTACATTTGATAAATGTTACACAGATGCAT
 TTGTGCATTGTAATACTCTGTAATTATACGGTGTAATATATGGGATTTAAAAAAGTG
 CTATCTTTCTATTTCAGTTAATTACAAACAGTTTTGTAACTCTTGTCTTTTAAATCTT

FIGURE 13

MGLQTTKWPSHGAFFLKSWLIISLGLYSQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPAELHNVQSVHTVYLYGNQLDEFFPMNLKPNVRVLHLQENNIQTI
SRAALAQLLKLLEELHLDNSISTVGVEDGAFREAI SLKLLFLSKNHLSSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLT KLKKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PNFCDCSIKWVTEWLKYPSSLNVRGFMCGPEQVRGMAVRELNMMNLLSCPTTTPGLPLFTTP
APSTASPTTQPPTLSIPNPSRSYTPPTPTTSKLPITPDWDGERVTPPIISERIQLSIHVND
TSIQVSWLSLFTVMAYKLTWVKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSFQIVSLNNDQLLK
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

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ACTTGGACGCAAGCGCGGGCGGAGACAGAGGCGACGACGAGCAAGCTGGGGCTCCGCTCTCCGCTCTCCACGAGCG
ATCTCCGAGGAGAGCGCGCGCCCTCTCGCGACGCGACGAGAGCGACGAGAGAACCCGGGTGGCTGGCCGCTGCC
TCGCTTCGACGGGCGCGCGGCTGCAGCCTTGCCCTCTTGCTCGCCTTGAAAATGCGAAAAGATGCTGCAGCGCT
GTTTTCGTGATCTTCGACAGCATGTCCTCTCTCCCTCCGAGCGCAGGAGCGGTCACGCTGGGAGTCCATCT
TAGGGGCGAGACGCTCGGACCGACCGCAGACGGCTCTTGAGAGTTCCTGTGAGAACAGCGGCGACAGC
TGTTTTCATTCATTGACAGCTTCGCACTGTCAACACCCATGACTGTCAAAAGTCGAAGGTTCATGTCGGGACA
CTTTGCAATTCTTGACATTTGTCCTGATGTCAACCGAGTGGGCTGCTCCAATATGGCGACAGCTGTCAAGAAT
AGTTTCTCCTCAGACACTTCAAAGGGAAGTGCAGGTGGAGCGTGCTGTCAAGAGGATCGCGCATCTGTCCAGC
GCGACCATGACTGGCTGSCCATCAGTATGCTCGAAACATGCATCTCAAAGACAGAGGGGCGCGCGCTCGT
GGGAGAAATGTGCCACGGGTCAATATGTCGACAGATGGGAGACATCAGGATCCGTGGCGGAGTGGCTGTA
AGGACCGGACAGCGGCATCTTAATTTTGCCATTGTTGGGCGAGGTAGACTTCAACACTTGAAGTCATTG
GGAGTGGACGCCCATGAGGACACATGTTCTTCTGTGGCCAACTTCAAGCCAGATTGAGACGCTGCACCTCGTGTCC
AGAGAAGTTGTGACCGGCCCATGTGTGCGACACCTGGAGCATTAAGTGTGCCACTTGTGACATAAACCTCTG
GCTCATAGCTTCGAGGTGCAAAACAGGCTACATTTCAATCTGGATCAGACAGCATTCGAGAAATCCAGGATGTGT
GTGCCATGGAGGACCAACTGTGAGACAGCTCTGTGTAATGTGGGTCGCTTCGTGTGCGACTGTACAGTG
GTCACGCGCTGCTGAGGATGGGAGAGAGTGTGTGGCTGTGACACTGTGCTCGAAGAAACACAGGATGTGAAC
ATGAGTGTGTAATGTGATGTGCTACTTCTTGGCAGTGGCATGAAGGATTGCTCTTACCCAGCATGAAAAC
CGTGACAGGAGATCAACTACTGTGACATGAAACCAACCGGGCTGTGAGCATGAGTGGCTCAACATGGAGGAGAG
ACTACTGCGCTGCCACCGTGGTCACTGTGACCAACCAATGGCAAACTCGAGCGAGTGGAGCCATGTGAC
ACGAGGACCAATGGCTGTGAGCAGCTGTGTGTAACACGGAGAGTCTTCTGCTGCGCAGTGTCAAGAGAGTCCC
TCATCAACAGGAGCACTCAAGACCTTCCGCGGTGGAAATGCTGCTGTGAGTAGAGTAAAGTTGGTTGAATACTCT
GTGTCAACATGGACACATCTTTGGGCTGCAGTGCTCTGGAGGACAGCTGCTCGCAGCGATGGGAAGACGCTGTG
CAGAAATGGACCTTTGTGCTCTTGCGGACACCGGTTGGAACATTGCTGTGTAGACGTGAAGATTCGTTTGTG
GCGAGCTCTTTGAAGGTATATATCTCCGTAAGATGGAAAACCTCGAGAAGAAAGATCTTGCCCAAGCTATAG
ACCATGCTGTGAAGTTTCTGTAAGTCAGTGACGACTACATACGTCGAGTGTGGAGGATTCGCGCTCG
TCGAGGATGGAAACGCTGCCAGGAAGAGATGTGCAAACTCAACCCACCTGCTGCGCAACCATCTGTGTGTTA
ATAATGGAAATCTACATCTGAAATCTCAGAGAGATTTGTTTAGCTGAGGACGGAAGCGTGCAGAAAT
GCACTGAAGGCCCATATGACCTTGTCTTTGTATCGATCGATCCAGAGTCTTGAGAGAGAAGATTTGAGATGT
TGAAGCAGTTTGTCACTGGAATTTATAGATTCCTTGACAATTTCCCGCAAGCGCTCGAGTGGGGCTGCTCAGT
ATTTCACACAGGCTCCACACAGAGTTCACTCTGAGAACAATCAACTCAGCCAGAGACATGAAAAGCGGTGGCCC
ACATGAAATCAGCGAAGAGGGCTCTATGATGGGCTGGCCCTGAACACATGTTTGAGAGAAATTTTACACAG
GAGAGGGGCTAGCGGCCCTTTCCAAAGGGTGCACGAGACGCCATTGTGTTCCACGACGCGGTCCAGGAT
ACGCTCTCCGAGTGGCGGATGAAGCCAGGSCAAATGGTATCACTATGTATGCTGTGGGGTAGGAAAAGCCATTG
AGGAGGACATCAAGAGATTGCTCTGAGCCCAACCAACAGCATCTTCTATCGGAAGACTTCAGACCAATGG
ATGAGATAGTGAAPAAACCTCAAGAAAGCAATCTGTGAAGCTCTAGAAGACTCCGATGGAAACAGGACTCTCCAG
CAGGGGACATGCAACAAACGGTCAACAGCCACAGAAATCTGAGCGAGTCACTATAAATATCAGAGACTTACTT
CTGTTTCTAATTTTGCACTGCAACACAGATATCTGTTTGTGAAGAGACCAATCTTTACGGTCTACACAAAGCTTT
CCCATTCACAAAACCTTTCAGGAAGCCCTTTTGAAGAAAAACAGATCAATCGAAATGTGAAAACCTTTAATGT
TCGAAACCTTGTCAAACAGGAAGATGAGAAAAATAACACAGCGCTTAGAAGAAATGACACAGAGAATGAAGGCC
TGAAGAACTCGCTTGAGATACAGATGAAGAAATGAAGATCGGACATCTTTGATGCTATGTATCAAGGATTAACA
GAACGAGCTGCAGAGGCCCAAGCTCAGGCTATGTGTAATACATAATGTGTGAAGTAAACCAATCAGTATCACT
GAACCTCGTTTTCGACAGCAAAAGACAGAAGTATACATACTGTATATAAATTTCTAGGAAAATAAATCT
TCGAATCTCAAGATGAATTTACAGGCTGAGAATGAATTAAGTATCAAGGTTATTTGTAAATATATGCTGGACAC
AACTGCTCTTCGCTCATCTCGCTGCTTAGTGTGCAATCTAATTTGACTATACATAAAGTTTGACAGCTTCTATTCT
CTTGAAGACACTGGCCATAGGAATTCGTGTTTTTTTGTATGGACTTACTTGTATATGTATATGATGATGTATG
CATAAATCATAGACATATGACTTGTGTGAACAAGTTGGATTTTTTATCAATAATATAAATTCACACTTCAG

FIGURE 15

MEKMLAGCFLLILGQIVLLPAEARERSRGRSISRGRHARTHPTQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSKTKRKRKSEVERAV
KRMRLHSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPDQDSVAEVAAKARD
TGILIFAIGVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSTVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTTCRIQDLCAMEDHNCQELCVNVPGSFVCQCYSGYA
LAEDGKRCAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCRINYCALKNKPGC
EHECVNMEESYYCRCHRGYTLDPNGKTC SRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPGHHVLRSDGKTCALKLSDCALGDHGCE
HSCVSSSEDSFVCQCFEGYILREDGKTCRRKDVCAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVCKSTHHGCEHICVNNGNSYICKCSBGFVLAEDGRRCKCTBGPIDLVPFVID
GSKSLGEENFEVVKQFVTGIIDSLTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKSGMTGLALKHMFERSFTQEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIBELQBIASEPTNKHLFYAEDFSTMDIEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTSEBPTTINIQLLSCSNFAVQHRYLFBEDNLLRSTQKLSHSTKPSGSPL
SEKHDQCKCENLIMFQNLANEVVRKLTQRLEEMTORMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

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FIGURE 16

GGAGCCGCCCTGGGTGTGAGGGCTCGGCTCCCGCGCAGCTCCGGCCGTCGCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGGCTGGCGCCCTGACTCCGTCCCGGCCAGGGAGGGC
CATGATTTCCTCCCGGGGCCCTGGTGACCAACTTGCTGCGGTTTTTGTTCCTGGGGGTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGGTGCAACTGCACCTTGCCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGGAAGTGGTGCTTCCAGCGTGGTACACCTTGACGGGGAGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTTGTGATGTGGTTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCTACATCAATGGGGTCACAACAAGCAAACCTGGAGTATCCTTGGTCTACTCC
ATGCCCTCCCGAACTGTCCCTGCGGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGGCCACAGCATCAAAACCT
TAGAACTCAATGTACTGGTTCCTCCAGCTCCTCCATCTGCGCTCTCCAGGGTGTGCCCCAT
GTGGGGGCAAAACGTGACCTTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTTCCATCCTTCCAGACTTTCTTTGCACCAGCATTAGATGTGATCCGTG
GGTCTTTAAGCCTCACCAACCTTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGTGGGTACCTGGTTGGAAGTGGGGTTGCTGGCTGGGTGGTCC
TCTTGTAACACCGCCGGGGCAAGGCCCTGGAGGAGCCAGCCAAATGATATCAAGGAGGATGCC
ATTGCTCCCGGACCTGCCCTGGCCCAAGAGCTCAGACACAATCTCCAAGATGGGACCTCT
TTCTCTGTGACCTCCGCACGAGCCCTCCGGCCACCCCATGGCCCTCCAGGCTGGTGCAT
TGACCCCCACGCCCAGTCTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACTCAACCAATATCCCCCATCCCTGGTGGGGTTTCTTCTCTGGCTTGAGCCG
CATGGGTGCTGTGCTGTGATGGTGCTGCCAGAGTCAAGCTGGCTCTCTGGTATTGATGAC
CCCACCACTCATTGGCTAAAGGATTTGGGGTCTCTCCTTCCTATAAGGGTCACTCTAGCAC
AGAGGCCTGAGTCATGGGAAAGAGTCAACATCCTGACCCTTAGTACTCTGCCCCCACTCTC
TTTACTGTGGGAAAACCATCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTTATGAAGCCAGCTG
CTGAAATTAGTACTCACCAAGAGTGAGGGGCAGAGACTTCCAGTCACTGAGTCTCCAGGC
CCCCTTGATCTGTACCCCAACCCTATCTAACACCACCCCTGGCTCCCACTCCAGTCCCTGT
ATTGATATAACCTGTGAGGCTGGCTTGGTTAGGTTTTACTGGGGCAGAGGATAGGGAATCTC
TTATTAATAAATAACATGAAATATGTGTTGTTTTCATTTGCAAATTTAAATAAGGATACATAA
TGTTTGATGAAAAA

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FIGURE 17

MISLPGLVLTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVFFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSQCSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGPGAA
VVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWKSSDTISKNGTL
SSVTSARALRPPHGPFRPGALTPTPSLSSQALPSPRLPTTDGAHPQIPISIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

100120.54320660

FIGURE 18

CGCCACCACCTGCGGCCACCGCCAATGAAACGCCTCCCGCTCCTAGTGGTTTTTTCCACTTTG
TTGAATTGTTCTTACTACAAAATTGCACCAAGACACCTTGTCTCCCAATGCAAAATGTGA
AATACGCAATGGAATTGAAGCCCTGCTATTGCAACATGGGATTTTCAGGAAATGGTGTCAAA
TTTGTGAAGATGATAATGAATGTGGAATTTAACTCAGTCCTGTGGCGAAAATGCTAATTGC
ACTAAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAAACCA
AGACAGGTTTATCATCAATGATGGAACCCGTCTGTATAGAAAAATGTGAATGCAAACTGCCATT
TAGATAATGTCGTATAGCTGCAAAATATTAATAAACTTTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTTGCTACAAGAAGTCTATAGAAATCTGTGACAGATCTTTCCACCAACAGA
TATAAATTACATATATAGAAATATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAA
CTATCTCAGCCAAGGACACCCCTTTCTAACTCAACTCTTACTGAATTTGTAAAAAACCGTGAAT
AATTTTGTTCAAAGGGATACATTTGTAGTTTGGGACAAGTTATCTGTGAATCATAGGAGA
ACATCTTACAAAACTCATGCACACTGTTGAACAAGCTACTTTAAGGATATCCAGAGCTTCC
AAAAGACCACAGAGTTTGATACAAATTCACCGGATATAGCTCTCAAGTTTCTTTTTGTAT
TCATATAACATGAAACATATTCTCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTCGACGTTGCATTTTATATTATA
AGAGTATTGTCTCTTTGCTTTCATCATCTGCAACTCTTATTGAAACCTCAAAATATTGAT
AATTCTGAAGAGGAGGAAAAGAGTCATATCTTCAGTAATTTCACTGCTCAATGAGCTCAAACCC
ACCCACATTATATGAACTTGAAAAAATAACATTTACATTAAGTCATCGAAAGGTCACAGATA
GGTATAGGAGTCTATGTGCATTTTGGAAATTAACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACT
GACACATTTTGCAATTTTGATGTCTCTGTGCTCTTCCATTGGTATTAAAGATTATAATATTC
TTACAGGATCACTCAACTAGGAATAATTAATTCATGATTTGTCTTGGCATATGCATTTT
ACCTCTGTGTTCTTTCAGTGAATTTCAAAGCACCAGGACAACAAATTCACAAAAATCTTTGCTG
TAGCCTATTCTTGTCTGATGTTGTTTTCTTGTGGGATCACTACAAATCAATTAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTTTAGCTGCTTTTGCATGGATGTGC
ATTGAAGGCATACATCTCTATCTCATTGTTGTGGGTGTCATCTACAACAAGGGATTTTTGCA
CAAGAATTTTTATATCTTTGGCTATCTAAGCCAGCCGCTGGTAGTTGGATTTTCCGACAGC
TAGGATACAGATATTATGGCACAACCAAGTATGTTGGCTTAGCACCGAAAAACAATTTATT
TGGAGTTTTATAGGACCAGCATGCCTAATCATTCTTGTAACTCTTGGCTTTTGGAGTCAT
CATATACAAAATTTTTCTGTCACACTGCAGGGTTGAAACCAAGAAGTTAGTTGCTTTGAGAACA
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTTCTGTTCTTCTCGGCACCACCTGGATCTTT
GGGTTCTCCATGTTGTGCAAGCATCAGTGGTTACAGCTTACCTCTTACAGTCAGCAATGC
TTTCCAGGGGATGTTCAATTTTTTATTCTGTGTGTTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTTCAAAAATGTCCCTGTTGTTTTGGATGTTTAAAGGTAACATAGAGAATG
GTGGATAATTACAACGTGCACAAAAATAAAAAATTCAGCTGTGGATGACCAATGTATAAAAA
TGACTCATCAAAATATCCAATTATTAATACTACTAGACAAAAAGTATTTTAAATCAGTTTTCT
GTTTATGCTATAGGAATGTAGATAATAAGGTAATAATTATGTATCATATAGATATACTATGT
TTTTCTATGTGAAATAGTTCTGTCAAAAAATAGTATTCAGATATTTGGAAAGTAATGGTT
CTCAGGAGTATATCATGCACGCCCAAGGAAGAATTTCTTTTAAACACGAGAAGTATATGAA
TGTCTTGAAGGAACCACTGGCTGTATTTCTGTGACCTGTTGCTTTGCTTTGCTTTGCTTCT
CCTACCACCTCGGTAATGAGCTCCATTACAGAAAGTGAACATAAGAGAATGAAGGGGCAGA
ATATCAACAGTGAAGGGGAATGATAAGATGTATTTGAATGAATGTTTCTTCTGTAGAC
TAGCTGAGAAATGTTGTACATAAAAAAAGAAATGAAGAACACATTTTACCATTTTGGAA
TTGTTCTGAACCTTAAATGTCCACTAAAAACAATAGACTTCTGTTTGTCAATCTGTTTCTT
TTTTCAATTTCTAAAAAATAAAAAAGGTTTACCTCCACAAATTGAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA

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FIGURE 19

MKRLPLLVPFSTLLNCSYTONCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIEVNVNANCHLDNVCI
NINKTLTKIRSIKEPVALLQEVYRNSVTDLSPTDIIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFEVKTVNNFVQRDTFVVWDKLSVNHRRTHLTCLMHTVEQATLRISQSFOKTTFT
NSTDIALKVPFFDSYNMKHIHPHMNMMDGDYINIFPKRKAAYDSNGNVAVAFLLYKYSIGPLLS
SSDNFLLPQNYNDSEEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDTRYRSLCAF
WNYSPTMNGSWSSEGCCLTYSNETHTSCRCNHLTHFAILLMSSGPGSIGIKDYNILTRITQLG
IIISLCLAI CIFTWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFCSTIAGL
LHYFFLAFAWMCI EGIHLYLIVVGVYINKGFLHKNFYIFGYLSPAVVVVGSAAALGYRYYGT
TKVCWLSTENNFISFIGPACLIILVNLLAPGVIIYKVFRTAGLKPEVSCFENIRSCARGA
LALLFLGTTWIFGVLVHVHASVVTAYLFTVSNAPQGMFIFLFLCVLSRKIQEYYRFLPKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAAATATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTTGCATTTTTATATTATAAGAGTAT
TGGTCCCTTTGCTTTCATCATCTGACAACTTCTTATTGAAACCTCAAATTTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTTCAGTAATTTAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTTACATTAAGTCAATCGAAAGGTCAAGATAGGTATA
GGAGTCTATGTGGCATTGGAATACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTTGCAATTTTGATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTTCACTGATTGTCTTGCCATATGCATTTTTACCTTC
TGGTTCTTCAGTGAAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCGCTGCGCGGTGGGGAGGAGTTCCCCGAAACCCGGCCG
 CTAAGCGAGGCCTCCTCTCCCGCAGATCCGAACGGCCCTGGGCGGGGTACCCCGGCTGGGA
 CAAGAAGCCGCGCCTGCTGCCCCGGGGCCGGGGAGGGGCTGGGGCTGGGGCCGGAGGCGG
 GGTGTGAGTGGGTGTGTGCGGGGGGCGGAGGCTTGATGCAATCCCGATAAGAAATGCTCGGG
 TGTCTTGGGCACCTACCCGTGGGGCCCGTAAGGCCTACTATATAAGGCTGCCGGCCCGGAG
 CCGCCGCGCCCTCAGAGCAGGAGCGCTGCGTCCAGGATCTAGGGCCACGACCATCCCAACCC
 GGCACTCAGAGCCCCGAGCGCATCCCGGTGCGCGCCAGCCCTCCCGACCCCCATCGCCGG
 AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGTGGTGGTCCAGTATGG
 ATCCTGCGCGGCCTCTGGCTGGCCGTGGCCGGGCGCCCTCGCCTTCTCGGACGCGGGGCC
 CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCGGCACCTGTACACCTCGGCCCCC
 ACGGGCTCTCCAGCTGTTCTGCGCATCCGTGCCGACGGCGTGTGGACTGCGCGCGGGGC
 CAGAGCGCGCAGATTTGTGTGAGATCAAGGCAGTCGCTCTGCGGACCGTGGCCATCAAGGG
 CGTGACAGCGTGCGGTACCTCTGCATGGGCGCCGACGGCAAGATGCAAGGGCTGCTTCAGT
 ACTCGGAGGAAGACTGTGCTTTCCGAGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
 TCCGAGAAGCACCGCCTCCCGGTCTCCCTGAGCAGTGCCAAACAGCGGCAGCTGTACAAGAA
 CAGAGGCTTTCTTCCACTCTCTCATTTCCCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
 AGGACCTCAGGGGCCACTTGGAATCTGACATGTTCTCTTCCGCCCTGGAGACCGACAGCATG
 GACCCATTGGGCTTGTACCCGGACTGGAGGCCGTGAGGAGTCCACAGCTTTGAGAATAACT
 GAGACCATGCCCCGGGCTCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGGACG
 TGCTTCTACAAGAACAGTCTGAGTCCACGTTCTGTTTAGCTTTAGGAAGAAACATCTAGAA
 GTTGTACATATTAGAGTTTTTCATTGGCAGTGCCAGTTTCTAGCCAAATAGACTTGTCTGAT
 CATAACATTGTAAGCCTGTAGCTTGCCAGCTGCTGCCCTGGGCCCCCATTTCTGCTCCCTCGA
 GGTGTGCTGGACAAGCTGTCTGCACGTCTCAGTTCTGCTTGAATACCTCCATCGATGGGGAAC
 TCACCTCCCTTTGGAATAATTCTTATGTCAAGCTGAAATCTCTAATTTTTTCTCATCACTTC
 CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTTAAATTTAGGAACAGGTGATCCACTCTGTA
 AAACAGCAGGTAAATTTCACTCAACCCCATGTGGGAATTGATCTATATCTCTACTTCCAGGG
 ACCATTTGCCCTTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGGCCCCACAG
 GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACTTGAGAAATCCCC
 CTGAGGCCAGTTCTGTCTATGGATGCTGTCTTGAGAATAACTTGCTGTCCCGGTGTCACTGC
 TTCCATCTCCCAGCCCCACAGCCCTCTGCCACCTCACATGCCCTCCCCATGGATTGGGGCCT
 CCCAGGCCCCCCACCTTATGTCAACCTGCACCTTCTGTTCAAAAATCAGGAAAAGAAAAGAT
 TTGAAGACCCCAAGTCTTGTCAATAACTTGCTGTGTGGAAGCAGCGGGGGAAGACCTAGAAC
 CCTTCCCCAGCACTTGGTTTTTCAACATGATATTATAGAGTAATTTATTTTGATATGTACA
 TCTCTTATTTTCTTACATTATTTATGCCCCCAAATATATTTATGTATGTAAGTGAGGTTTG
 TTTGTATATTAAATGGAGTTTGGTTGT

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FIGURE 22

M R S G C V V V H W I L A G L W L A V A G R P L A F S D A G P H V H Y G W G D P I R L R H L Y T S G P H G L S S C F L R I
R A D G V V D C A R G Q S A H S L L E I K A V A L R T V A I K G V H S V R Y L C M G A D G K M Q G L L Q Y S E E D C A F E E
E I R P D G Y N V Y R S E K H R L P V S L S S A K Q R Q L Y K N R G F L P L S H F L P M L P M V P E E P E D L R G H L E S D
M F S S P L E T D S M D P F G L V T G L E A V R S P S F E K

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

00002515-071001
F00120-51920660

FIGURE 23

CCCAGAAGTTCAAGGGCCCCCGGCCCTCTGCGCTCCTGCCGCCGGGACCCCTCGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGGAAGATGCGCAGGAGGAGCCGCCACCGCCTCCTCCTGCTG
CTGCTGCGCTACCTGGTGGTGCCTGGGCTATCATAAGGCCTATGGGTTTTCTGCCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTTAGCCTGCAAAACCCCAA
AGAAGACTGTTTCCTCCAGATTAGAGTGGAAGAACTGGGTGGAGTGTCTCCTTTGTCTAC
TATCAACAGACTCTTCAAGGTGATTTTAAAAATCGAGCTGAGATGATAGATTTCAATATCCG
GATCAAAAATGTGACAAGAAGTGATGCGGGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAAACTGGAAGAGGATACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCTCTTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGGAATCCAGCTCCTGAATACACATGGTTTAAAGGATGGCATCCGTTTGCTAGAAA
ATCCCAGACTTGGCTCCCAAAGCACCAACAGCTCATACACAATGAATACAAAACTGGAAC
CTGCAATTTAATACTGTTTCCAAACTGGCACTGGAGAATATTCTGTGAAGCCCGCAATTC
TGTTGGATATCGCAGGTGTCCTGGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTTAGTGATTTCCGTTTGTGGCCTTGGTGTATGCTAT
GCTCAGAGGAAAGGCTACTTTTCAAAGAAACCTCCTTCCAGAAGAGTAATTCTTCATCTAA
AGCCACGACAATGAGTGAAAAATGTGCAGTGGCTCACGCCTGTAATCCAGCACTTTGGAAGG
CCGCGGCGGGCGGATCACGAGGTGAGGAGTTCTAGACCACTCTGGCCAATATGGTGAAACCC
CATCTCTACTAAAATAAAAAATTAGCTGGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTTGAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAATAAATA
AATAAAATACTGGTTTTTACCTGTAGAATTCTTACAATAAATATAGCTTGATATTC

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKDQQVVTAVEYQEAILACKTPKKTVSSRLE
WKKLGRSVSFVYYQQTQLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGIRLLENPRLGSQST
NSSYTMNTKTGTQLQFNTVSKLDTGEYSCEARNNSVGYYRRCPGKRMQVDDLNISGIIAAVVVVA
LVISVCGLGVCYAQRKGYFSKETSFOKSNSSSKATMTSENVQWLTPVIPALWKAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

09902615-071001

FIGURE 25

GACATCGGAGGTGGGCTAGCACTGAACTGCTTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAGATGTTGGGGCAACATTATTATTAAACATGCTCCACAGCCCGGACCTGGGCAT
CATGCTGCTATTCTTCGCAAAATACCTGAAGAAGCATGGGATTTAAATATTTTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTTCAAAGAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACTTCTCTTCCAATATGCATGACATTTTGGACAATG
CAATTGTGGCACTGGCACTTATTTTCAGTGAAGAAAACTTTGTGGTTCTATGGCATTCATCA
TTTGACAAATGCAAGCATCTTCCTTATCAATCAGCTCCTATTGAACCTTACTAGCACTGACTG
TGGAAATCCTTAAAGGGCCATTACATTTCTGAAGAAGAAAGCTAAGATTGAAGGACATGCCACT
CCGAATTCATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGCTGTGAAATCAGGCCTTGGTTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTTAGGTCCTTTAACTTTCCACGCCAGATTGCC
AGCTAACACACAGATTCTTCTCCTACAGACTAACATATTGCAAAAAATGGAATACTCCACAG
ACTTTCAGTAAACCTTACTGGCCTGGATTATCTCAAAACAATTTATCTTCAGTCACCAAT
ATTAATGTAAAAAGATGCCCTCAGCTCCTTTCTGTGTACCTAGAGGAAAAACAACTTACTGA
ATCTGCTGAAAAATGTCTGTCCGAACCTGAGCAACTTACAAGAACTCTATATTAATCACAACT
TGCTTTCTACAATTTCACTTGGAGCCTTTATTGGCCTACATAAATCTTCTTCGACTTCAATCTC
AATTCAATAGATTGCAGATGATCAACAGTAAGTGGTTTGATGCTCTTCCAATCTAGAGAT
TCTGATGATTGGGGAAAAATCCAATTATCAGAATCAAGACATGAACCTTAAAGCCTCTTATCA
ATCTTGCGAGCCTGGTTATAGCTGGTATAAACTCACAGAAATACAGATAACGCCTTGGTT
GGACTGGAAAACTTAGAAAGCATCTCTTTTACGATAACAGGCCTATTAAAGTACCCCATGT
TGCTCTTCAAAAGTTGTAATCTCAAAATTTTGGATCTAAATAAAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTTAGCAATATGCTACACTTAAAGAGTTGGGGATAAAATAATATGCCT
GAGCTGATTTCCATCGATAGTCTTGCTGTGGATAACCTGCGAGATTTAAGAAAAATAGAAGC
TACTAACACCCCTAGATTGTCTTACATTACCCCAATGCATTTTTCAGACTCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGTCTATCCGTTG
GATGAACATGAACAAAACCAACATTCGATTATCGGAGCCAGATTCACTGTTTTGCGTGGACC
CACCTGAATTTCCAAGTGCAGAATGTTCCGGCAAGTGCAATTTCAGGGAACATGATGGAAATTTGT
CTCCCTCTTATAGCTCCTGAGAGCTTTCCCTTCTAATCTAAATGTAGAAGCTGGAGCATGTG
TTCCCTTTCACTGTAGAGCTACTGCAGAACCAAGCCTGAAATCTACTGGATAACACCTTCTG
GTCAAAACTCTTGCTTAATACCTGCAGACAAGTTCTATGTCCATTCTGAGGGGAACACTA
GATATAAATGGCGTAACTCCCAAGAAGGGGGTTTATATACTTGTATAGCAACTAACCTTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTTTCCACAAGATAACAATG
GCTCTTTGAATATTTAAATAAGAGATATTCAAGCCAATTCAGTTTGGTGTCTCGGAAAGCA
AGTTCTAAAAATTTCAAACTCTAGTGTAAATGGACAGCCTTTGTCAAGACTGAAAAATTTCTCA
TGCTGCGCAAGTGTCTGCAATACCATCTGATGTCAAGGTATATAATCTTACTACTCTGAATC
CATCAACTGAGTATAAAATTTGATTGTATATCCCACTATCTCAGAAAAACAGAAAAAAA
TGTGTAATGTCAACCACCAAGGTTTGCACCTGTATCAAAAAGAGTATGAAAAGAATAATAC
CAACACTTGTGGCTGTCTTGGAGGCCTTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCTCTCTCCGAAATGAACCTGTGATGGTGGACACAGCTATGTGAGGAATTAATCTACAG
AAACCAACCTTTGCATTAGGTGAGCTTTATCTCCTCTGTATAATCTCTGGGAAGCAGGAAA
AGAAAAAGTACATCACTGAAAGTAAAGCAACTGTTATAGGTTTACCAACAAATATGTCTT
AAAAACCAAGGAAACCTACTCCAAAAATGAAC

09902615-071001

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKKVCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQIILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKMPQLLSVYLE
ENKLTTELPEKCLSELNLQELYINHNLSTISPGAFIGLHNLRLHLNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVLIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNNLKFLDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESIMLNSNALSALYHGHTIESLPNLKEISIHSPIRC
DCVIRWMNMNKTNIIRFMEPDSLFCVDPPEFQGNVRQVHFRDMMEICPLIAPESFPSNLNV
EAGSYVSFHCRTATAEPQPEIYIWITPSGQKLENTLTDFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGADLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAfv
KTENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTTLMACLGGLGIIGVICLISCLSPENMCDGGHSYVRNYLQKPTFALGELYPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

0902615-071001
10070-5122660

FIGURE 27

GCCCGGGACTGGCGCAAGGTGCCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTGATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTTGTCTCTCCTCTGGG
GGTTTTAAATGTACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTTCCCTCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCCAATGAAATTTTAAAG
ACCTCCATCAACTGAGAGTTCTCAACCTGTCCAAAAATGGCATTGAGTTTATCGATGAGCAT
GCCTTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCTTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCCTCAATGCTGC
CAACGACGCTGACCTTTGTAACTCCCTAAAAAACTACCGATTATGCCATGTCTGGTCACCA
TGTTTGGCTGGTTCACTATGGTGATCTCATATGTGGTATATTATGTGAGGCAAAATCAGGAG
GATGCCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTATAGTGTCCAACTGACTGTCAATTGAGAAAGAAAGAAA
GTAGTTTGCATTGCAGTAGAAATAAGTGGTTTACTTCTCCCATCCATTGTAACATTTGAA
ACTTTGTATTTCACTTTTTTTTGAATTATGCCACTGCTGAACTTTTAACAAACACTACAACA
TAAATAATTTGAGTTTAGGTGATCCACCCCTTAATTGTACCCCGATGGTATATTTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTTAATAATGAAATTTATTTTTTT
AATTTAAAGCAAATAAAGCTTAACCTTTGAACCATGGGAAAAAAAAAAAAAAAAAAAAACA

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FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRFFL
NAANDADLCNLPKKT TDYAMLVTMFGWFTMVISYVVVYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

090615-07001
120120-1192060

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCCCGAGATGCGAGGTGAGCAAGAGGATGCTGGCGGGG
GGCGTGAGGAGCATGCCCCAGCCCCCTCCTGGCCCTGCTGGCAGCCCCATCCTCCTGCTGGTGCT
GGGCTCAGTCTGTGAGGCTCGGCCACGGGCTGCCCGCCCGTCCGAGTGCTCCGCCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTTGTGGCAGTCCCCGAGGGGATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCAGCATCAAACCGCTCAACCAGGACGAGTTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAAACATCGTGAGCGCCGTGGAGCCCCGGCG
CCTTCAACAACCTCTTCAACCTCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC
CGCCTAGGCGCTTTCACCTGGCCCTCAGCAACCTGACCAAGCAGGACATCAGCGAGAAACAAGAT
CGTTATCCTACTGGACTACATGTTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCTCACCGCGCCTTCAGCGGCCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCCATCCCCACCGAGGCGCTGTCCCACTGCAACGGCT
CATCGTCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTTGGAGATCTCCCACTGGCCCTACTTGGACACCATGACACCCAAC
TGCCCTTACGGCCTCAACCTGACGTCCCTTGCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCATCA
GCACCATTTAGGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCCGTGGTGGAGCCCTATGCCCTTCCGCGGCCTCAACTACCTGCGCGTGCTCAA
TGTCTCTGGCAACCAGCTGACCACACTGGAGGAATCAGTCTTCCACTCGGTGGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGGCTCAACTTCAACCGGCAGCAGCCACGTGCGCCACGCCCGAGTTTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTTCACTGCGCGCGCG
CCCGCATCCGGGACCGCAAGGCCAGCAGGTGTTTGTGGACGAGGGCCACACGGTGCAAGTTT
GTGTGCCGGGCGGATGGCGACCCGCCGCCCATCTCTGGCTCTCACCCGAAAGCACTT
GGTCTCAGCCAAGAGCAATGGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCCAGGTACAGGACAAACCGCACGTACCTGTGCATCGCGGCCAACCGGGCGGCAACGAC
TCCATGCCCGCCCACTGCATGTGCGCAGCTACTGCCCGACTGGCCCCATCAGCCCAACAA
GACCTTCGCTTTCATCTCAAACGAGCCGGGCGAGGGAGAGGCCAACAGACCCCGCGCCACTG
TGCCCTTCCCTTTCGACATCAAGACCTCATCATCGCCACCACCATGGGCTTCACTCTCTTTC
CTGGGCGTCTGCTCTTCTTCTGGCTGGTGCTGTTCTCTGGAGCCGGGCAAGGGCAACAC
AAAGCACACATCGAGTCGAGTATGTGCCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCGCCCCGCAAGTTCAACATGAAGATGATATGAGGCGGGGGGGGGGGGAGGACCCCGG
GGCGGGCGGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCAGTCTTCCCACTC
CTCCCTACCCTTCTACACAGTTCTCTTTCTCCCTCCGCTCCGTCCCTGCTGCCCCCCG
CCAGCCCTCACCACCTGCCCTCTTCTACAGGACCTCAGAAGCCAGACCTGGGGACCCCA
CCTACACAGGGGCAATTGACAGACTGGAGTTGAAAGCCGACGAAACCGACACGCGGCAGAGTCA
ATAATTCAATAAAAAAGTTACGAACCTTCTCTGTAACTTGGGTTTCAATAATTATGGATTTT
TATGAAACTTGAATAATAAAAAAGAGAAAAAACTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 30

MQVSKRMLAGGVSRMPSPLLACWQPIILLVLGSLVSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPTETRLDLLGKNRIKTLNQDEFASPHLELELNENIVSAVEPGAFFNNLFLNRLTL
GLRSNRLKLIPLGVFTGLSNLTQDISENKIVILLDYMFQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTISIPTALSHLHGLIVLRLRHLNINAIIRDYSFKRLYRLKVLEISH
WPYLDTMTFPCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLEHL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLLEESVFHSVGNLETLILDSNPLA
CDCRLLWVFRRLWRLNFRNQOPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIAILWLSPRKHLVSAKSNGRLTVPDGTLEVRYAQVQDNQTYL
CIAANAGGNDMPAHLHVRYSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCLVLLFLWSRGKNTKHNIIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

09902615-071001

FIGURE 31

CCCACGCGTCCGCACCTCGGCCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTTCGGTCAAC
ATCGTAGTCCACCCCCCTCCCATCCCCAGCCCCCGGGGATTAGGCTCGCCAGCGCCAGCC
AGGGAGCCGGCCGGGAAGCGCGAATGGGGGCCCCAGCCGCCTCGTCTCTGCTCCTGCTCCTGC
TGTTCCGCTGCTGCTGGGCGCCCGGCGGGGCCAACCTCTCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAAAGTGGTGGCTGGTGGCACCGTGGTGTCAAGTGCCAAAGTGAAAAGATCA
CGAGGACTCATCCCTGCAATGGTCTAACCTGCTCAGCAGACTCTCTACTTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTGAGCTGGTTACCTCTACGCCCCACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCACAGAAGCCCATCATCACTGGTT
ATAAATCTTCATTACGGGAAAAAGACACAGCCACCTAAACTGTCACTCTTCTGGGAGCAAG
CCTGCAGCCCCGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTGACGAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTCTCTGTGAACCATGAATCTTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTTCCCTTCTCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCGCTACAAGGCCTACTACACCTCAATGTTAATGACCCAGTCCGGTGCCCT
CCTCCTCCAGCACCTACCAGCCATCATCGGTGGGATCGTGGCTTTCATTGTCTTCTGCTG
CTCATCATGCTCATCTTCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGCGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGGACGACAAGAAGGAATATTTCATCTAGAGGCGCTGCCCACTTCTCTGC
GCCCCCAGGGGCCCTGTGGGGACTGTGGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGAGGGCCGCCCTCCCGCTTGCTCCCCAGCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGTACTCGGTTTGAATGGGAGGGAGGAGGGCGGGGGAGGGGAGGG
TTGCCCTCAGCCCTTTCGTTGGCTTCTGCAATTTGGGTTATTATTATTTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAACA

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020312

Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCAACCCCTTTTCTTCTCTTTCTGCTG
CTTCGGACATTTGGAGCACTAAATGAACCTGTAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTTGTGATGAGATCGGGGATGAATTGCTCGCTTTAAAAATGCTGCTTTGGATTCTGTT
GCTGGAGACGCTCTCTTTGTTTGTCCGCTGGAACGTTACAGGGGACGTTTGCAAGAGAGAAGA
TCTGTTCTCTGCAATGAGATAGAAAGGGACCTACACGTAGACTGTGAAAAAAGGGCTTCACA
AGCTTCGAGCCTTTCACTGCCCGGACTTCCGAGTTTACCATTATTCTGTCATGGCAATTC
CCTCACTCGACTTTTCCCTTAATGAGTTTCGCTAACCTTTATAATGCGGTTAGTTTGCAATGG
AAAAAATGCTTCGATGAATCGTTCCGGGGCTTTTCTGGGGCTGCAGCTGGTGGAAAGG
CTGCACATCAACAACAAGATCAAGTCTTTTCGAAAGCAGACTTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTTATACGAGATATAGACCCGGGGGCTTCAGG
ACTTGAACAAGCTGGAGGTCTCATTTTAAATGACAATCTCATCAGCACCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATCACCCACTCGACCTCCGGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCTT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAACACATTCCCAAGAAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCACAGACTGCAGGTAAGAAGCTCAATGAAC
ACCGGAACAGCACTGTGTCTCTTTGAAAAACCGAGTGGATTAGTCTCCGGGCGCCCTCG
CCCAAGAAGAGACCTTTGCTCCTGGACCCCTGCCAACTCCTTTCAAGACAAATGGGCAAGAG
GATCATGCCACACAGGGCTGCTCCAAACCGAGGTACAAAGATCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGAGGGTAGCTCCAGGAACAAACCTTAGCTAACAC
GTTTACCTGCGCTGGGGGCTGCGAGCTGCGACCATCCAGGGTTCGGGTTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTTGGCTGATTTGAAGCCCAAGCTCTCTAACGTGACGGA
GCTTTTCCACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTTGTGGATTACAAGA
ACCTCATCTCTGTTGGATCTGGGCAACAATAACATCGCTACTGTAGAGAACAACACTTTCAAG
AACCTTTTGGACCTCAGGTGGCTATACATGGATAGCAATTAACCTGCACACGCTGTCCCGGGA
GAAATTCGGGGGCTGCCAAAACCTAGAGTACCTGAACGTTGGAGTACAACGCTATCCAGCTCA
TCCTCCCGGGCACTTTCAATGCCATGCCAAACCTGAGGATCCTCATTCTCAACAACAACCTG
CTGAGGTCCTGCTGCTGTGGACGTGTTGCTGCGGTCTCGCTCTCTAAACTCAGCCTGCACAA
CAATTACTCTCATGTACCTCCCGGTGGCAGGGGTGCTGGACCACTTAACCTCCATCATCCAGA
TAGACCTCCACGGAACCCCTGGGAGTGCTCCTGCACAAATGTGCTCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTATGCTCCTCTCCAAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCACGTTAACTTCGCACAGTAAAAACAGCACTGGGTTGGCGGAGACCGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGGTGCTCATCTCGTGTTGTTGCCCTTCAAGCAGTGGGCA
GTTTGTACCTTCGGCTTCAACGTTGGGATGCTCGTGTATCTCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAATCCTCCGCGTCCGAGATTAATTCCCTACAGACAGCTGTG
GACTCTTCTACTGGCACAATGGGCCCTTACAACGCAGATGGGGCCACAGAGTGATAGCTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCCAATAGGGGAGGCGAGAGGAAGCGG
ATACACTCTTCCCCACCGCAGCCACCCGGGGCTGGAGGGGCTGTACCCAAATCCCGCG
CCATCAGCCTGGATGGGCATAAGTAGATAAAATAACTGTGAGCTGCACAACCGAAGGGGCT
GACCCCTTACTTACTTCCCTCTTGAACAAAGAGCAGACTGTGGAGAGCTGTGGAGAGCGCA
GCCAGCTCGCTCTTGTGAGAGCCCCCTTTTGACAGAAAGCCAGCAGACCTGCTGGAAG
AACTGACAGTCCCTCGCCCTCGGCCCGGGGCTGTGGGGTTGGATGGCCGCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTAATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCTGTGTGGCTACGCAGGATGGGCAGTTGCACGAAGGCATGAATGTAT
GTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGDVCKEIKCSCNEIEGDLHVDCEKKGFTSLQRFTAPT SQFYH
LFLHGNLSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFLGLQLVKRLHINNKKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAQDLNKLLEVLILNDNLISTLPANVFQYVPI THLDLRG
NRLKTLPLYEEVLEQIPGIAEILLEDNPWDCTCDLLSLKEWLENI PKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPAQEETFAPGPLPTPFKTINGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSPLCPGGCSCDHIPGSLKMNCNNRNVSSIADLKP
KLSNVQELFLRDNKIHSIRKSHFVDYKNLILLDLGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLLEYLNVYNAIQILIPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNNYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTSHNSYLDTSRVSI SVL
VPGLLL VFVTSAFTVVGMLVFI LRNRKRKRDRANDSSASEINSLQTVCDSSYWHNGPYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577, .
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

09902615-071001

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGCGCCAGCTGTGTTCTTGACCCCAGAATAACTCAGGGC
 TGCACCGGGCCTGGCAGCGCTCCGCACACATTTCTGTGCGGGCCTAAGGGAAACTGTTGGC
 CGCTGGGCCCGCGGGGGGATTCTTGCCAGTTGGGGGGTCCGTGCGGAGCGAGGGCGGAGGGG
 AAGGAGGGGGAAACCGGGTTGGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
 AGCTCTGCGTCTCTGAGCGGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCAGGGGCTCAG
 AGAATGAGGGCGCGCTTCGCCCCTGTGCCCTCTTGGCAGGCGCTCTGGCCCGGGCGGGCGG
 CGGCGAACACCCCACTGCGCAGCGTGTGCGTGTCTGCGCCTCGGGGGCCTGCTACAGCCTGCG
 ACCACGCTACATGAAGCGGCAGGCGGCGGAGGAGGCTGCGTCTGCGAGGTGGGGCGCTC
 AGCACCCTGCGTGCAGGGCGCGGAGCTGCGCGCTGTGCTCGCGCTCTGCGGGCAGGCGCCAGG
 GCGCCGAGGGGGCTCCAAAGACCTGTGTTCTGGGTGCGCACTGAGCGCAGGCGTTCCCACT
 GCACCTTGAGAACGAGCCTTTGCGGGGTTTCTCCTGGCTGTCTCCGACCCCGCGGTCTC
 GAAAGCGACACGCTGCAGTGGGTGGAGAGCCCCAACGCTCTGCAACCGCGCGAGATGCGC
 GGTACTCCAGGCCACCGGTGGGGTTCGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
 GCGCAACCGGTACCTGTGTCAAGTACCAGTTTGAGGTCTTGTGTCTTGCGCCGCGCCCCGGG
 GCGCGCTCTAACTTGAGCTATCGCGCGCCCTTCCAGCTGCACAGCGCGCTCTGGAATTGAG
 TCCACCTGGGACCGAGGTGAGTGCCTCTGCGGGGACAGCTCCCGATCTCAGTTACTTGCA
 TCGCGGACGAAATCGCGCTCGCTGGGACAACTCTCGGGCGATGTGTTGTCTCTGCCCC
 GGGAGGTACCTCCGTGCTGGCAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
 CTTTGCCTGCGAATGTGCTACGGGCTTCGAGCTGGGGAAGGACGGCGCTCTTGTGTGACCA
 GTGGGGAAGGACAGCCGACCTTTGGGGGACCGGGGTGCCACACAGGCGCCCGCGGCCACT
 GCAACCAGCCCGCTGCCGAGAGAACATGGCCAACTCAGGTCGACGAGAAGCTGGGAGAGAC
 ACCACTTGTCCCTGAACAAGACAAATTCAGTAACATCTATTCCCTGAGATTCCTCGATGGGGAT
 CACAGAGCAGATGTCTACCTTCAAATGTCCCTTCAAGCCGAGTCAAAGGCCACTATCACC
 CCATCAGGGAGCGTGATTGCCAAGTTTAATTCTACGACTTCCCTTGCCACTCTCAGGCTTT
 CGACTCTCTCTGCGCGTGGTCTTCATATTTGTGAGCACAGCAGTAGTAGTGTGTTGATCT
 TGACCATGACAGTACTGGGGCTTGTCAAGCTCTGCTTTTACGAAAGCCCTCTTCCAGCCA
 AGGAAGGAGTCTATGGGCCCGCGGGCTTGAGAGTGATCCTGAGCCCGCTGCTTTGGGCTC
 CAGTTCTGCACATTGCACAAACATGGGGTGAAGTCTGGGGACTGTGATCTGCGGGACAGAG
 CAGAGGGTGACCTTGTGTCGGGAGTCCCTCTTGGCTCTAGTGATGCAATAGGAAACAGGGGA
 CATGGGCACTCCTGTGAACAGTTTTTTCACTTTTGTGATGAACCGGGGAACCAAGAGGAACCTTAC
 TTTGTGTAACGACAAATTTCTGCAGAAATCCCCCTTCTCTAAATTCCTTTTACTCCACTGAG
 GAGCTAAATCAGAACTGCACACTCCTTCCCTGATGATAGAGGAAGTGAAGTGCCCTTAGGA
 TGGTGATACTGGGGGACCGGGTAGTGCTGGGGAGAGATATTTTCTTATGTTTATTTCGGAGAA
 TTTGGAGAAGTGATTGAACCTTTTCAAGACATTGGAACAAATAGAACAATATATATTTACA
 TTAATAAATAATTTCTACCAAAATGGAAGGAAATGTTCTATGTTGTTTCAAGCTAGGAGTAT
 ATTGGTTCGAAATCCCAGGGAAAAAATAAAAAATAAAAAATAAAGGATTGTTGAT

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FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAE LRAVLALLRAGPGPGGGSKDLLFWVALEERRRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLC PAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCFG
RYLRAGKCAELPNCLDDLGGFACECATGFELGKDGRCVTS GEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMTVLGLVKLCFHESPSSQPR
KESMGPPGLESDPEPAALGSSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGGATTACAGCAGTGGCCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
 CGTCGAGTCAGACGGCACCATAATCGCCTTTAAAAGTGCCCTCCGCCCTGCCGCGCGCGTATC
 CCCCGGCTACCTGGGCCCGCCCCGCGCGGTGCGCGCGTGAGAGGGAGCGCGCGGGCAGCCGA
 GCGCCGCTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGCGGTGTGAGCGCGGTGGGTGCGGA
 GGGCGCTGTGTGCCGCGCGCGCGCGTGGGGTGCAAAACCCGAGCGTCTACGCTGGC**ATGA**
 GGGGCGCGAACCGCTGGGCGCCACTCTGCCCTGCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
 CAGCAGTCCCCAGAGAGACCTGTTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
 TATTGGCAGTGAAGGTTTTCTGGAGTGTAACCTCCAAATAGCAAAATGTACTTGGAAAAATCA
 CAGTTCCCGAAGSAAAAGTAGTCGTTCTCAATTTCCGATTTCATAGACCTCGAGAGTGACAAAC
 CTGTGCCGCTATGACTTTGTGGATGTGTACAAATGGCCATGCCAATGGCCAGCGCATTGGCCG
 CTTCTGTGGCACTTTCCGGCCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
 TGATTTCTGATGCCAACACAGCTGGCAATGGCTTCATGGCCATGTTCTCCGCTGCTGAACCA
 AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTTCCGGCTCTTTTAAAC
 CCCCAACTGGCCAGACCGGGATTACCTGCGAGGAGTCACTGTGTGTGGCACATTGTAGCCCC
 CAAAGAATCAGCTTATAGAATTAAGTTTGAGAAGTTTGATGTGGAGCGAGATAACTACTGCG
 CGATATGATTATGTGGCTGTGTTAATGGCGGGGAAGTCAACGATGCTAGAAGAATTGGAAA
 GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTCTTATTCAGT
 TTTTATCAGACTTAAGTTTAACTGCAGATGGGTTTATTGGTCACTACATATTCAGGCCAAAA
 AAACCTGCCTACAACCTACAGAACAGCCTGTCAACCCACATTCCCTGTAACCACGGGTTTAAA
 ACCCACCCTGGCCCTGTGTCAACAAAAGTGTAGACGGACGGGACTCTGGAGGGCAATTATT
 GTTCAAGTGACTTTGTATTAGCCGGCACGTATCACAAACCATCACTCGCGATGGGAGTTTG
 CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTTGGCGATTTCAGCAGGCGGG
 CAAGAACATGAGTGCCAGGCTGACTGTGCTGTGAAGCAGTGCCCTCTCCTCAGAAGAGGTC
 TAAATTACATTATTATGGGCCAAGTAGGTGAAGATGGGCGAGGCAAAATCATGCCAAACAGC
 TTTATCATGATGTTCAAGACCAAGAATCAGAAGCTCCTGGATGCCTTAAAAAATAAGCAATG
TTAACAGTGAACCTGTGTCCATTTAAGCTGTATTCTGCCATTGCCTTTGAAAGATCTATGTTCT
 TCTCAGTAGAAAAAATACTTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
 GACTGGTTGACTCTTCACATGATGGAGGTATGAGGCCCTCCGAGATAGCTGAGGGAAGTTCTT
 TGCCTGCTGTGAGAGGAGCAGCTATCTGATTGGAACCTGCCGACTTAGTGCGGTGATAGGA
 AGCTAAAGTGTCAAGCGTTGACAGCTTGGAAGCGTTTATTTATACATCTCTGTAAAAAGGAT
 ATTTTGAATTTAGTTGTGTGAAGATGTCAAAAAAGATTTTAGAAGTGCAATATTTATAGT
 GTTATTGTGTTTACCTTCAAGCCTTTGCCCTGAGGTGTTACAATCTGTCTTGGCTTTTCTA
 AATCAATGCTTAATAAAATATTTTTAAAGGAAAAAAAAAAAA

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FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVTTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVLNFRFIDLESNDLCRYDFVDVYNHANGQRIGRPCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSENNELLI
QFLSDLSLTADGFIGHYIFRPKKLPPTTEQPVTTTFPVTITGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITITITRDGSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

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FIGURE 39

CGGACGCGTGGGCGGACGCGTGGGCGGCCACGGCGCCCGCGGGCTGGGGCGGTCGCTTCTT
CCTTCTCCGTGGCTACGAGGGTCCCAGCCTGGGTAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGGCCTCAGCCTCTTCTCAACCTCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTCTATACCTG
CCGGGGACTGGTTGACAGCTTTAAAGGGCCTGGAGAGAACCATCCGGGACAACCTTTGGAG
GTGGAAACACTGTCCTGGGAGGAAGAGAATTTGTCCAAATACAAAGACAGTGAGACCCGCTG
GTAGAGGTGCTGGAGGGTGTGTGCAGCAAGTCAGACTTCGAGTGCCACCGCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTTTCACAAGCAGCAGGAGGCCCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTTCGGGGCCCTCTGTC
CTTCCCTGTCTGGGGGAACAGAGAGGCCCTGCGGTGGCTACGGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGGTGAGGCCTGTGGCC
AGTGTGGCCTTGGCTACTTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTTCGGCTTGT
TTTGGCCCCCTGTGCCCGATGCTCAGGACCTGAGGAATCAAAGTGTGTCATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGTAGACATTGATGAGTGTGGCACAGAGGGAGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAAACCGAGGGCGGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGTGCTGCAGCAGATGTTCTTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCGACTTGGTGTTCACCGCCATCTTCATTGGGGCTGTGGCGGCCATG
ACTGGCTACTGGTTGTGTCAGAGCGCAGTGACCGTGTGCTGGAGGGCTTCATCAAGGGCAGATA
ATCGCGGCCACCACTGTAGGACCTCTCTCCACCCACGCTGCCCCAGAGCTTGGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTTATTTTGGAGTGGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCCGGGCAGACAAGCCCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTTACCTGGCGGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTTTCCTTAATGGTGGCTGCTAGAGCTTTGGCCCTGCTTAGGATTAGGTG
GTCTTCACAGGGGTGGGGCCATCACAGCTCCCTCCTGCCAGCTGCATGCTGCCAGTTCCTGT
TCTGTGTTCAACCATCCCCACCCCATTGCCACTTATTTATTCATCTCAGGAAATAAGA
AAGGCTTTGAAAGTTAAAAA

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FIGURE 40

MAPWPPKGLVPAVLWGLSLFLNLP GPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCCPAGTFGFSCLPCPGGTERPCGGYGQCEGEGTRGGSGHCDQAG
YGGACGQCGLGYFEARNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCQADQFCVNTESYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDLVVLQQMFFG
IIICALATLAAKGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGGCACCTCTGGGTGTTGCCCCTGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGGCAGCCTGCTGCGGCAGCTGCAGCTCAAAGAGGT
GCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTTCCAGCAGAGC
TTCCGAGAGGTTGGCCGGCAGGTTCTTGCGTTGGAGGCCAGCACACCTGCTGGTGTTCGG
CATGGAGCAGCGGTGCGCGCCCAACAGCGAGCTGGTGCAGGCCGTGCTGCGGCTCTTCCAGG
AGCCGGTCCCCAAGGCCGCTGTCACAGGCACGGGCGGTGTCCCCGCGCAGCGCCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCGCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCCAAGCTGGTCCGCTTTGCCCTCGCAGGGGGC
GCCAGCCGGGCTTGGGGAGCCCCAGCTGGAGCTGCACACCTGGACCTTGGGGACTATGGAG
CTCAGGGCGACTGTGACCTGAAGCACCAATGACCAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGGATGAAGTGGGCCGAGAACTGGGTGCTGGAGCCCCCGGGCTT
CCTGGCTTATGAGTGTGTGGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCCTCAAGTGGC
CGTTTCTGGGGCCTCGACAGTGCATCGCCTCGGAGACTGACTCGCTGCCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCCAGCCATTAGCGCCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTGTTTCTGAAGTGTTCGAGGGTACCAGGAGAGCTG
GCGATGACTGAACTGCTGATGGACAAATGCTCTGTGCTCTCTAGTGAGCCCTGAATTTGCTT
CCTCTGACAAATTACCTCACCTAATTTTGTCTTCTCAGGAATGAGAATCTTTGGCCACTGGA
GAGCCCTTGCTCAGTTTTCTCTATTCTTATTATTCAGTGCATATATCTAAGCACTTACAT
GTGGAGATACTGTAACTGAGGGCAGAAAGCCCANTGTGTCATTGTTTACTTGTCTGTGAC
TGGATCTGGGCTAAAGTCTCCACCACCACCTCTGGACCTAAGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAAACACATTTTATTCT
AAAA

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FIGURE 42

MQPLWLCWALWVLPLASPGAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFSQSFRVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRSLSPRSARARVTVEWLRVRDDGSNRTSLIDSRVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQVSVQREHLGPLASGAHKLVRFASQGAPAGLGEPLQLHTLTLGLDYGAG
GDGCDPEAPMTGETRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCTCRQPPEALAFKWP
LGFRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSASDGAIVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

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FIGURE 43

GTCTGTTCCAGGAGTCCTTCGGCGGCTGTTGTGTCACTGGCCTGATCGCGAATGGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTGCCTCTTCATATTGGCGATCCTGTTGTGCTCCCTGG
CATTGGGCAGTGTTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTTCTCTCCCGTGTGGAGTGGAAGTTTGACCA
AGGAGACACCACCAGACTCGTTTGTCTATAATAACAAGATCACAGCTTCCTATGAGGACCGGG
TGACCTTCTTGCCAACTGGTATCACCTTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGGCAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAAACATCCCCCTCCTCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAAGATGGTTCCCCACCTTCTGAATACACCTGGTTCAAAGAT
GGGATAGTGATGCCTACGAATCCCAAAAGCACCCGTGCCTTCAGCAACTCTTCCTATGTCTCT
GAATCCCAACAGGAGAGCTGGTCTTTGATCCCCGTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGGTTCATCGTGCCAGCCGTCTTTGTAAACCTGATTCTCCTGGGAAT
CTTGTTTTTGGCATCTGGTTTGCTATAGCCGAGGCCACTTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGTCCTTACT
CAGGTGCTACCGGACTCTGGCCCCGTGATGTCTGTAGTTTCACAGGATGCCTTATTTGTCTTC
TACACCCACAGGGCCCCCTACTTCTTCGGATGTGTTTTTAATAATGTGAGCTATGTGCCCC
ATCCTCCTTCATGCCCTCCCCTCCCTTTCTCTACCACTGCTGAGTGGCCTGGAACCTGTTTAAA
GTGTTTATTTCCCATTTCTTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTTGAATAGGTATCTTGAGCTTGGTTCTGGGCTCTTCTCCTGTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGTTTGG
TGATGACACTGGGGTCCTTCCATCTCTGGGGCCCACTCTCTTCTGTCTTCCCATGGGAAGTG
CCACTGGGATCCCTCTGCCCTGTCTCTCTGAATACAAGCTGACTGACATTGACTGTGTCTGT
GGAAAATGGGAGCTCTTGTGTGGAGAGCATAGTAAATTTTCAGAGAACTTGAAGCCAAAAG
GATTTAAACCGCTGCTCTAAAGAAAAGAAAACCTGGAGGCTGGGCGCAGTGGCTCACGCCTG
TAATCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGGAGTTGGGATCAGCCTGACCA
ACATGGAGAAACCTACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGATGCCTGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAGAGCAAAAACCTCCAGCTCAAAAAAAAAAAAAAAAAA

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FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLS CAYS GFSSPRVEW
KFDQGD TTRLVCYNNKITASYEDRVTF LPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTCSEQDGSPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGT PMT SNAVRMEAVERNVGVIVA AVLVTLI
LLGILVFGIWFAYS SRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

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FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGGACAGCATGAGCGGCGGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGGCTCTGGGCCTGGCGCTGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCGCGCCGCGAGCCCGCTTTCCACCCGACCTCTGCCCAGGCCGAGGCCCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAAGTGGCTTATGCGTGCCCCCTACCTGG
CGCTGCGACAGGGACTTTGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAAGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCACCGCCCCCTGGCCTCCCCTGCCCCCTGCACCGGCGTCA
GTGACTGCTCTGGGGGAATGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTCGGCTGTGGAACCAATGAGATCCTCCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTACCTCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCTGGAGAGTGTCCCCCTCTGTGCGGAATGCCACATCCTC
CTCTGCCGAGACCAGTCTGGAAGCCCAACTGCCTATGGGGTTATTGCAGTGTCTGCGGTGC
TCAGTGCAAGCCTGGTACCCGCCACCTCCTCCTTTGTCTGCTGCTCCGAGCCAGGAGCGC
CTCCGCCCACTGGGGTTACTGGTGGCCATGAAGGAGTCCCTGTGCTGTGAGAACAGAAGAC
CTCGCTGCCCCTGAGGACAAGCACTTGCCACCACCGTCACTCAGCCCTGGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGGAACTGCCACAGCCAGAAGTGA
GGGCTGGCCCCAGGCAGTCCCAGGGGAGTAGAACGGCCCTGTGCTTAAGACACTCCCTGTCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

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Signal sequence:

Transmembrane domain:

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCCACGCGTCCGGTCTCGTCTCGTCTCGCGCAGCGGCGGCAGCAGAGGTGCGGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAGGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGATATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGTTTCAGCTGGCGCTGTGCTTCGGCCCTGCACAGCTCACGGGCGGGTT
CGATGACCTTCAAGTGTGTCTGACCCCGGCATTCCCAGAAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTTCTTTGAAGGCTCTGTAGCCCGATTCTACTGCCAAGACGGATTCAAGTGAAG
GGCGCTACAAAGAGACTGTGTTTGAAGCATTTTAAATGAACCTTAGGCTGGATCCCAGTGA
TAATTCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTCATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTGCATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCATTATGTGCGGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTCTAATGGCTATGTAACATCTCTGAGC
TCCAGACCTCCTTCCGGTGGGGACTGTGATCTCCTATCGTGCTTTCCCGGATTTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCTGCCAGCCACCCCGTG
CCTTGCTCTGGAAGCCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTTCTGCT
GCCACCCGCGGCTTGTGAGCGCTACAACCACGGAACGTGGTGGAGTTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTACGGCAACCAAGTGTGCTGCTGGTGCTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCCACTTTCCCCCAGGGGGCCCTCCCGGAG
TTCAGCAGTGAACCTGACTTTGTGGTGGTAGACGGCGTGCCCGTCATGCTCCCGTCTTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCTTAGGCCCCGGGTACATGGCCTCTGTGGGCCAG
GGCTGCCCTTACCCGTGGAGCAGCAGAGCCCCCAGCATACCCCGGCTCAGGGGACACGGA
CACAGGCCAGGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTTCTGAGCTGCTCCAAA
GTCTGTATTACCTCCCAGGTGCCAAGAGAGCACCCACCTGCTTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGAGGTGGCATCCACCAGCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTTAAGAAACTGATTTGATTAAAAAATTTCCCAAAGTGTCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTTCTTCTCTTGGTTTTAGACAAATGTAAACAA
AGCTCTGATCCTTAAATTTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTTGATCAAGTC
CTGTTTCTTCTTGACACAGACTGATTAAAAATTTAAAGNAAAAA

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FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKGATKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSPPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFTATSVLLVLLLVILARMFQTKFAHFPPRGPPRSSSSDPDFVVVD
GVPVMLPSYDEAVSGLSALGPGYMASVGGQCPLPVDQSPPAYPGSGD TDTGPGESETCDS
VSGSELLQSLYSPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

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FIGURE 49

CCCACGCGTCCGCTCCGCGCCCTCCCCCGCCTCCCGTGCGGTCCGTGCGGTGGCCTAGAGA
TGCTGCTGCCGCGGTTGCAGTTGTGCGGCACGCCTCTGCCGCCAGCCCGCTCCACCGCCGT
AGCGCCCCGAGTGTGCGGGGGCGCACCCGAGTCCGGGCCATGAGGCCGGGAACCGCGCTACAGG
CCGTGCTGCTGGCCGTGCTGCTGGTGGGGCTGCGGGCCGCGACGGGTGCGCTGCTGAGTGCC
TCGGATTTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTTA
TAAAGTCATTACTTCCATGATACTTCTCGAAGACTGAACTTTGAGGAAGCCAAAGAAGCCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAACTGATAGAA
AAGTTCATTGAAAACCTCTTGCCATCTGATGGTGACTTCTGGATTGGGCTCAGGAGGCGTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTTATGCTTGGACTGATGGCAGCATAT
CACAATTTAGGAACTGGTATGTGGATGAGCCGTCCTGCGGCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTTCAATTTGCAATATTTCTGATGAGAAACCAGCAGTTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAAGTAGAGAAGCTGCCTTGAATCTGGCCCTACAT
CCTAATCCCCAGCATTCCCCCTTCTCTCTCTTGTGGTCACCACAGTTGTATGTTGGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCTAGCACAAAGAAGCAACACACCATC
TGGCCCTCTCTCACCAGGGAACAGCCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTTCAATCCGAGTGTGTT
CGGGAGAAGCCACTCCCGATGACATGTCTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGGTTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTTATGA
GTTCTCCCAGACCAAATGGGGAGGAGTAAGGAGTCTGGATGGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTTCTATAAGGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCCGTG
GGATGAGCATGTGGTCCCCACGACCTCCTGTTGGACCCCCACGTTTTGGCTGTATCCTTTAT
CCCAGCCAGTCATCCAGCTCGACCTATGAGAAGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAAATGTCACTTGGTTGGTTGTATCTAACTTTTAAGGGACAGAGCTTTACCTG
GCAGTGATAAAGATGGGCTGTGGAGCTTGGAAAACCACCTCTGTTTTCTTGCTCTATACAG
CAGCAGATATTATCATACAGACAGAAAATCCAGAATCTTTTCAAAGCCACATATGGTAGCACAG
GTTGGCTGTGCATCGGCAATTCTCATATCTGTTTTTTCAAAGAATAAAATCAATAAAGA
GCAGGAAAAA

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FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSI ESEDEQK LIEKFIENLLPSD GDFWIGLRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNNFICKY
SDEKPAVPSREAEGETELTTPVLPEETQEEDAKKTFKESREALNLAYILIPSIPLLLLLLV
VTTVVCWVWICRKRKREQDPSTKKOHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSESGFVTLVSVEGSGFVTNDIYEFSPDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

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FIGURE 51

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GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGCTGAAGGGCTGGATGTACGC
ATCCGCAAGTTCCCGCGACTTGGGGGCGCCCGCTGAGCCCCGGGCGCCGCAAGACTTGT
GTTTGCTCTCTGCAGCCTCAACCCGAGGGGAGCGAGGGCCTACCACCAATGATCACTGGTGT
GTTGAGCATGCGCTTGTGGACCCAGTGGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCGATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTCGTGTTTCGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAAACCCAGCTATTAGAGGTCCCACCCCAAACCTC
AGTTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCTGAAGGGGGGCATGTTTGCTGGGCGAGTGACCAAGTGGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTTC
TTTACCAACCTTCAACCCACAGGAGGTCTTTATTCGTTCCTAACAATTTTCGGAATCTG
GAGTCCACCCGTTGTTTGCTGGCTGGGCTTTTCCAGTGTGAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTGAGAACTCTTGATCCCAACTACCAAGCTGCTGGAGCCCTGA
GGCAGAGAACCAGAGGCCGGAGGCAGACTGCCTCTTTACAGCCAGGAATCTCAGAGGATTTG
AAAAAGGTGAAGGACAGGATGGGCATTGACAGTAGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCGAGCAGGCACACAACCTCCCAAGCTGCCCATGTGAAGAGATTTG
CACGGATGATCGAAAGAGAGCTGTGGACACATCCTTGATACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCCGACAAGATCAGAAAGCTGTATCTCTATGCGGCTCATGATG
TGACCTTCATACCGCTCTTAATGACCCTGGGGATTTTGACCACAAATGGCCACCCTTTGCT
GTTGACCTGACCATGGAACCTTACCAGCACCTGGAATCTAAGGAGTGGTTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCGAGAGGTTGCCCTGATGGGCTCTGCCCGCTGGACATGT
TCTTGAATGCCATGTCACTTTATACCTTAAGCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAATGAAGAGTAACTGATTTATAAAAGCAGGATGTGTTGATT
TTAAATAAAGTGCCCTTTATACAATG

FIGURE 52

MITGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLAGLFCQCKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLLKKVKDRMGIDSSDKVD
FFILLDNVAAEQAHNLPSCPMLKRFAIRIEQRAVDTSLYILPKEDRESLQMAVGPFLLHILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLMLTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSIVYTLSPKEYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

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FIGURE 53

CTCCTCTTAACATACTTGCAGCTAAAACTAAATATTGCTGCTTGGGGACCTCCTTCTAGCCT
TAAATTTTCAGCTCATCACCTTCACCTGCCTTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCTTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGCACC GTGTGTGATG
ACGGCTGGGACATTAAAGGACGTGGCTGTGTGTGTGCGGGAGCTGGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTTGTATGAGCCACCAGCAGAAAAAGAGCAAAAGGTCTCTATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATACATTGGCTCAGTGTGAGCAAGAAGAGTTTATG
ATTGTTACATGATGAAGATGCTGGGGCATCGTGTGAGAACCAGAGAGCTCTTTCTCCCCA
GTCCAGAGGGGTGTCAGGCTGGCTGACGGCCCTGGGCATTGCAAGGGACGCGTGAAGTGAA
GCACCAGAACCAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGGCCGCAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCTTCA
GGATTGCCCTTCTGGGCCCTGGGGGAAGAACACCTGCAACCATGATGAAGACACGTGGGTCG
AATGTGAAGATCCCTTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGGCTCTGTCTGTGATGACAAC TGGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCTCCCTCCTTCAGAGACCGGA
AATGCTATGGCCCTGGGGTTGGCCGCATCTGGCTGGATAATGTTCTGTGCTCAGGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTTGGGGGTTTCACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTTACTGTCTACATGACTGCATGGGATGAACACTGATCT
TCTTCTGCCCTTGGACTGGGACTTATACTTGGTGCCCTGATTCTCAGGCCTTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTTGGAAC TACATCA
CCACCTTTCTATGTCTCCACATTGCACACAGCAGATTCCAGCCTCCATAATGTGTGTAT
CAACTACTTTAAATACATTCTCACACACACACACACACACACACACACACACACAT
CACCATTGTCTGTTTCTCTGAAGAACTCTGACAAAATACAGATTTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTTTAAAGGATAAATTTTCTGAATTTGGTTATGGGGTTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTTCTGGTAACTTTATTTACAATAATAAAGATAGCA
TATGTGTTCAAA

000265-0100

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGGLHRCGRVEVEQKQWGTVCDDGWDIKDVAVLC
RELGC GAASGTPSGILYEPPAEKEQKVLIIQSVSCTGTEDTLAQCEQEVEYDCSHDEDAGASC
ENPESSFSVPVEGVRLADGPGHCKGRVEVKHQNQWYTVTCQTGWSLRAAKVVCRLGCGRAVL
TQKRCNKHAYGRKPIWLSQMSCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLC SGRLEVLHKG VVGSV CDDNWGEKEDQVVC KQLGCGKSLSPSPFRDRKCYGPGVGRIWL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

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FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACGCGTCCGCGGACGCGTGGGCGGACGCGTGGGCCGGCTACCAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTTCGGCTGCCTGGG
CGTCTTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGGAAGGCCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGCGCCACCTCAGGGCTGGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTTGGTGACCTTCGACC
TCACAGACTCTGGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTTGGCTATGTC
GACATACTTGTCAACAATGCTGGGATCAGCTACCGTGGTACCATCATGGACACCACAGTGGA
TGTGGACAAGAGGGTTCATGGAGACAAACTACTTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCCTTTTCGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTTCTTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTCTGTAATGCCATCACCGCGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCACAGCCCAGGGCCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCCTTGGCTGTTTATCTTCGAA
CTCTGGCTCCTGGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGACGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTTGTTGAGACTTTAATGGAGATTGTCTCACAGTGGG
AAAGACTGAAGAAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATCAAAAACGACAACA
AGCTTCTTCCAGGGTGAGGGGAAACACTTAAGGAATAAATATGGAGCTGGGGTTTAAACAT
AAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAAAAAGGGCGGCCGCACTTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTTTATTGCAGCTTATAATGGTTAC

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FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKECAKVFYAAGA
KLVLGCRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDRVMETNYFGPVALTKALLPSMIKRRQGHIVAIISSIQGMKSI
PFRSAYAASKHATQAFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRVGVMDTTT
AQGRSPVEVAQDVLAAVGGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

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FIGURE 57

CCCACGCGTCCGCTGGTGTAGATCGAGCAACCCTCTAAAAGCAGTTTAGAGTGGTAAAAAA
AAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTTCTTCTGGACATCCTC
CTGCTTCTCCGTTACTGATCGTCTGCTCCCTAGAGTCTTCGTGAAGCTTTTATTCTCTAA
GAGGAGAAAATCAGTCACCGCGGAAATCGTGTGATTACAGGAGCTGGGCATGGAATTGGGA
GACTGACTGCCTATGAATTTGCTAAACTTAAAAGCAAGCTGGTCTCTGGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAAATGCAAGGGACTGGGTGCCAAGGTCATACCTTTGT
GGTAGACTGCAGCAACCAGAGAAGATATTTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTTAGTAAATAATGCTGGTGTAGTCTATACATCAGATTTGTTTGTCTACA
CAAGATCCTCAGATTGAAAAGACTTTTGAAGTTAATGTACTTGCACATTTCTGGACTACAAA
GGCATTCTCTCTGCAATGACGAAGAATAACCATGGCCATATTGTCACTGTGGCTTCGGCAG
CTGGACATGTCTCGGTCCCTTCTTACTGGCTTACTGTTCAAGCAAGTTTGCTGCTGTTGGA
TTTCATAAACTTTGACAGATGAACTGGCTGCCTTACAAATACTGGAGTCAAAACAACATG
TCTGTGTCTAATTTGCTAAACACTGGCTTCATCAAAATCCAAGTACAAGTTTGGGACCCAA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCAATGGGATTCTGACTGAGCAGAAGATG
ATTTTTATTCCATCTTCTATAGCTTTTTTAACAACATTGGAAAGGATCCTTCCTGAGCGTTT
CCTGGCAGTTTTAAACGAAAAATCAGTGTTAAGTTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATTAAGCACCTAGTTTTCTGAAAACGTATTTACCAGGTTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTTAATGTTTGAACCTCTGTTTTTTCTAATTATCCCCATTCTTCAATA
TCATTTTTGAGGCTTTGGCAGTCTTCATTTACTACCCTTGTTCTTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAATACCTTTAGAGGTGACTTTAAGGAAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAATAATTTCCAAGATTATTTGTGGCTCACCTGAAGGCTTTGCAA
AATTTGTACCATAACCGTTTATTTAACATATATTTTTATTTTGATGCACTTAAATTTTGT
ATAATTTGTGTTTCTTTTTCTGTTCTACATAAAATCAGAACTTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGTGGTATTTTCAATGAATATCATGAACCTCTCAATGGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTTCTGAGAGATACCTCACATTCCAATGCCAAACATTTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTTAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

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FIGURE 58

MKFLLDILLLLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKS
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEENVLAHFWTTKAFLPAMTKNNHGHIIVTVASAAGHVSVPFLLAYC
SSKFAAVGFGFKTLTDELAALQITGVKITCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRMLH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

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FIGURE 59

CCCACGCGTCCGCGGACGCGTGGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGGGCTC
AGGGAGGAGCACCGACTGCGCCGCACCTTGAGAGATGTTGGTGCCATGTGGAAGGTGATTG
TTTCGCTGGTCCTGTTGATGCCTGGCCCTGTGATGGGCTGTTTCGCTCCCTATACAGAAGT
GTTTCCATGCCACCTAAGGGAGACTCAGGACAGCCATTATTTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAAGGAAGAGAATTGAGTTTGGTCGGCCCTTTCCCGAGGACTGAACATGA
AGAGTTATGCGGGCTTCTCACCGTGAATAAGACTTACAACAGCAACCTCTTCTTCTGGTTT
TTCCCGAGTCAGATACAGCCAGAAGATGCCCGAGTAGTTCTCTGGCTACAGGGTGGGCCGGG
AGGTTCTATCCATGTTTGGACTCTTTGTGGAACATGGGCCCTTATGTTGTCAACAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATACCCACGGATATGCAGTCAATGAGGACGATGT
AGCACGGGATTATACAGTGCCTAATTACAGTTTTCAGATATTTCTCTGAATATAAAAAATA
ATGACTTTTATGTCACTGGGGAGTCTTATGCAGGAAATATGTGCCAGCCATTGACACCTC
ATCCATTCCCCTAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCCGAATCAATTATAGGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAAGCAAAAAAGTACTTCCAGAAGCAGTGCCATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTTGGAGCCTTTGAAATACTGGATAAACTACTAGATGGCGACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAAGCTTTTTGCGGT
GCACGGAACCTGAGGATCAGCTTTACTATGTGAAATTTTTGTCACTCCCGAGGTTGAGACAA
GCCATCCACGTGGGGAATCAGACTTTTAAATGATGGAACATAGTTGAAAAGTACTTGCGAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTAACTGAAATCATGAATAATTATAAGGTTCTGA
TCTACAATGGCCAACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTTGATGGGC
ATGGACTGGAAGGATCCAGGAATACAAGAAGGCAGAAAAAAGTTTGGAAAGATCTTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCCATCAGGTAATTATTC
GAGGTGGAGGACATATTTTACCCTATGACCAGCCTCTGAGAGCTTTTGACATGATTAAATCGA
TTCATTTATGGAAGGATGGGATCCTTATGTTGGATAAACTACCTTCCCAAAAGAGAACAT
CAGAGGTTTTATTGCTGAAAAGAAAATTCGTAATAACAGAAAATGTATAGGAATAAAAAA
TTATCTTTTATATCTGCAAGATTTTTTTCATCAATAAAATATATCTTGAACCAAGTGAGC
TTTTGTTTTTGGGGGGAGATGTTTACTACAAAATTAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAGATGTATAAATGA
AATTTTAGGGCTTGAATAGGAAGTTTTAATTCTTCTAAGAGTAAGTGAAAAGTGCAAGTTG
TAACAAACAAAGCTGAACATCTTTTCTGCCAATAACAGAAGTTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATTGGATAAGAATAGCTCAATTATCCCAATAAATGGATGAAGCTATAA
TAGTTTTTGGGAAAAGATTCTCAATGTATAAAGTCTTAGAACAAAAGATTCTTTGAAATA
AAAAATATTATATAAAAGTAAAAAATA

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FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDGQPLFLTPYIEAGKIQKGRELSL
VGPPFGLNMKSYAGFLTIVNKTYNSNLFWFPPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDPFWTTTSLMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQT
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSLSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEAFIILDKLLDGLTSDPSYFQNVGT
CSNYYNPLRCTEPEDQLYVVKFLSLPEVRQAIHVGNQTFNDGTIVEKYLRDQTVSVKPWLT
EIMNNYKVLIIYNGQLDIIVAAALTEERSLMGMDWKGSGEYKKAEEKVWKIFKSDSEVAGYIRQ
AGDFHQVVIIRGGGHILPYDQPLRAFDMINRFIYGKGDWPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

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FIGURE 61

CGAGGGCTTTTCCGGCTCCGGAATGGCACATGTGGGAATCCAGTCTTGTGTGGCTACAACAT
TTTTCCCTTTCTTAAACAAGTTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTCTCTCTT
GCTGGAGAAGAAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCTCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTTTGTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGGAGGGCTGCCTAAACAAGCTTTCAAAAAACAGGAGCGACTTCCACTGGGCTGGGAT
AAGACGTGCCGGTAGGATAGGGAAGACTGGGTTTAGTCTTAATATCAAATTGACTTGCTGGG
TGAACCTTCAACAGCCTTTTAACTCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTTGTAAAATAAAATTTTAAAAAAGCAAGTATTTTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCTGAACTTCCTAAGAGGGAGAAAGTATGTTAAAAATA
GAAAAACCAAATGCAAGAAGGAGGAGACTCACAGAGCTAAACCAGGATGCGGGACCTGGGT
AGGCCAGCCTCTTTGCTCCTCCCGAAATTATTTTGGTCTGACCACCTGTCCTTGTGTTTT
GCAGAATCATGTGAGGGCCAAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCTCAGTGGTCTGGGTGCTGCTGGCCCCCAGCAGCCGGC
ATGCTTCAGTTTCAGCCTCTTCCACTCTGAGAATCGTGACTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGGCGTCTATGTGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCTCAGGTGGCTCATAAGACAGGGCCAGAGAGGACAACAAGTCTCGTTACCCG
CCCCCTCATCGTGCAGCCCTGCAGCGAAGTGCTCACCTTCAACAACATGTCAACAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTCTACACGGGGGTCTGCA
AGCTGCTGCGGCTGGATGACCTCTTATCCTGCTGGTGGAGCCATCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCCACCATGTACGGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGAAGCTCTTCATCGGCACGGCTGTGGATGGGAAGCAGGATTACTCCCGACCTGTCCA
GCCGGAAGCTGCCCGGACCCCTGAGTCTCAGCCATGCTCAGTATGAGCTACACAGCGAT
TTTGTCTCCTCTCTCATCAAGATCCCTTCAGACACCTGGGCCCTGGTCTCCCACTTTGACAT
CTTCTACATCTACGGCTTTGCTAGTGGGGCTTTGTCTACTTTTCTACTGTCCAGCCCGAGA
CCCCTGAGGGGTGGGCCATCAACTCCGCTGGAGACCTCTTCTACACCTCACGCATCGTGCGG
CTCTGCAAGGATGACCCCAAGTTCCACTCATACGTGTCCTTGCCCTTCGGCTGCACCCGGGC
CGGGGTGGAATACCGCCTCTGCAGGCTGCTTACCTGGCCAAGCCTGGGGACTCACTGGCCC
AGGCCTTCAATATCACAGCCAGGACGATGTACTCTTTGCGATCTTCTCCAAAGGGCAGAAG
CAGTATCACCAACCCGCCGATGACTCTGCCCTGTGTGCCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCTGCAGTCTTGCTACAGGGCAGGGCACTTGGAGCTCAACTGGC
TGCTGGGGAAGGACGTCCAGTGCACGAAGGCGCCTGTCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCCTGACCTGTACACCAC
CAGCAGGACCGCATGACCTCTGTGGCCTCCTACGTTTACAAAGGCTGAGCGTGGTTTGTG
TGGGACTCAAGAGTGGCAGCTGAAAAGGTAAGAGTCTATGAGTTCAGATGCTCCAATGCC
ATTCACTTCTCAGCAAAAGAGTCCCTCTTGGAAAGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTTATTTTCTGGGGAAACAAAGGTGAATGGGGAGGTAAGAAGGGGTAAATTTTGTG
ACTTAGCTCTAGCTACTTTCCTCCAGCCATCAGTCATTGGGTATGTAAAGGATGCAAGCGTA
TTTCAATATTTCCCAAACTTTAAGAAAAAAGCTTTAAGAAGGTACATCTGCAAAAGCAA

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FIGURE 62

MGTLGQASLFAPPNGNYFWSHSAFCFAESCEGQPGKVEQMSTHRSRLTTAAPLSMEQRQPWP
RALEVDSSRSVLLSVVWVLLAPPAAGMPQFSTFHSNDRDWTFNHLTVHQGTGAVYVGAINRV
YKLTGNLTIQVAHKTGPEEDNKSRYPLIVQPCSEVLTLTNNVNKLLIIDYSENRLACGSL
YQGVCKLLRLDDLFILVEPSHKKEHYLSSVNKTGTMYGVIVRSEGEDGKLFIGTAVDQKQDY
FTLSSRKLRPRDPSSAMLDYELHSDFVSSLIKIPSDTLALVSHFDIFYIYGFASSGGFVYFL
TVQPETPEGVAINSAAGDLFYTSRIVRLCKDDPKFHSYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAAQAFNITSQDDVLFALFISKGQKQYHHPDDSAFCFPIRAINLQIKERLQSCYQGGEGN
LELNWLLGKDVQCTKAPVIPDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLLKKVRVYEFRCSSNAIHLSSKESLLEGSYWWRFNRYQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

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FIGURE 63

AGGCTCCCGCGCGGCTGAGTGCAGTACTGGAGTGGGAACCCGGGTCCCCGCGCTTAGAGAAACACGCGATGACCA
 CGTGGAGCCTCCGCGGAGGCGCGGCCGCGCAGCTGGGACTCCTGCTGCTGGTGGTCTTTGGGGCTTCTGGTGCTCC
 GCAGGCTGGACTGGAGCAACCTGGTCCCTCTGCGGCTCCGCCATCGACAGCTGGGGCTGGAGGCAAGGGCTGGA
 ACTTCTAGCTGAGGAGATTCCACCTTCTGGATCTTCGGGGGCTCCATCCACTATTTCCGTGTGCCACGGGAGTACT
 GGAGGGACCGCTGCTGAAGATGAAGGCTTGGCTTGAACACCTTCCACCTATGTTCGTGGAACTTCTGCTG
 AGCCAGAAAGAGGCAAAATTTGACTTCTCTGGGAACCTGGAGCTGGAGGCTTCTGCTGCTGATGGCCGACAGAGATCG
 GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCAGTGAATGGACCTCGGGGGCTTGCCCACTGGCTACT
 TCAAGAACCTTGGCATGAGGCTGAGGACAACTTACAAGGGCTTCAACGAAGCAGTGGACCTTTATTTTGACACACC
 TGATGTCCAGGGTGTGCCACTCCAGTCAAGCGTGGGGGACCTATCATTGCCGTGCAAGTGGAGAATGAATATG
 GTTCTCTATAATAAGACCCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTTGGAACTGC
 TCCTGACTTCAAGCAACCAAGGATGGGCTGAGCAAGGGGATGTCCAGGGAGTCTTGCCCACTCAACTTGCAT
 CAACACACGAGCTGCAGTACTGACCACCTTCTCTTCAACGTCCAGGGGACTCAGCCCAAGATGGTGTGAGT
 ACTGGACGGGGTGGTTTGACTCTGTTGGGGAGGCCCTCACATATCTTGGATTCTTCTGAGGTTTGAAGAACCGTGT
 CTGCCATTGTGGACGCCGGCTCCTCCATCAACCTCTACATGTTCCAGGAGGCCAACCTTTGGCTTATGAATG
 GAGCCATGCACTTCCATGACTACAAGTCAGATGTACACAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
 ATTACACGGCCAAGTACATGAAGCTTCGAGACTTCTTCGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
 ACCTTCTTCCCAAGATGCCGTATGAGCCCTTAACGCCAGTCTTGACTCTCTCTGTTGGGACGCCCTCAAGTACC
 TCGGGTACATTCTCTATGAGACCAGCATCACTCGTCTGGCATCTCAGTGGCCACGTGCATATGTCGGGGGACGG
 TGTTTGTGAACACAGTATCCATAGGATTCTTGGACTACAAGCAACCAAGATTTGCTGTCCCTGATCCAGGGTT
 ACACCGTGTGAGGATCTTGGTGGAATCTGTGGCGAGTCAACTATGGGGAGAATATTGATGACACCGGCAAG
 GCTTAAATTTGAATCTCTATCTGAATGATTACCCCTGAAAACTTCAAGATCTATAGCTCGGATTAAGAAGAA
 GCTTCTTCAAGGTTTGGGCTCGGCTGGACAATGGNGTTCCCTCCAGAAACCAACCATCTGCTCTTCTTGG
 GTAGCTTGTCCATCAGCTTCAACGCCCTTGTGACACCTTCTGAGCTGGAGGCTGGAGAAGGGGTTGTATTCA
 TCAATGGCCAGAACTTGGACCTTACCTGGAACATTGGACCCCAAGACCTTTACCTCCAGGCTCCTGTGTA
 GCAGCGGAATCAACACCGCTCATCGTTTGTAGGAGACGATGGCGGCCCTGCATACAGTTTCAAGAAACCCCCC
 ACTCGGCGAGAACAGTACATTAAGTGAAGCGGTGGCACCCCTCTGCTGTGTGCCAGTGGGAGACTGCCGCTC
 CTCTTGAACCTGAAGCCTGGTGGCTGCTGCCCAACCTCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGG
 ACTGGGGCTACAGTCTGCCCTCTGCTCAGCTCAAAACCTTAAGCCTTGGAGGAAAGGTGGGATGGCTTGGGCC
 TGGCTTTGTGATGATGGCTTTCTTACAGCCCTGCTCTTGTGCGGAGGCTGTGGGCTGTCTTAGGGTGGGAGC
 AGCTAATCAGATCGCCAGCCTTTGGCCCTCAGAAAAAGTGTGAAACGTGCCCTTGACACGGACGTCAAGCCC
 TGCAGCATCTGCTGGACTCAGCGTGTCTTTTGTGTTCTTGGGAGGCTTGGCCACATCCCTCATGGCCCAT
 TTTATCCCCGAAATCTTGGTGTGTACCAAGTGTAGAGGTTGGGGAAGGGGTGTCTACCTGAGCTGACTTTGT
 TCTCTTCAACCTTCTGAGCCTTCTTGGGATTCTGGAAGGAATCGGCGTGAAGAACATGTGACTTCCCTT
 TCCCTTCCCACTCGTGTCTTCCACAGGGTGAAGGCTGGGCTGGAGAACAGAAATCTTCACTCCCTGCTCTTCC
 CAAGTTAGCAGGTGTCTCTGGTGTTCAGTGAGGAGCATGTGAGTCTTGGCAGAACCATGGCCCATGTCTGCA
 CATCCAGGGAGGAGAGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCATGGCCATGTCTGCAATCC
 AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCTTGGCAGAAGCATGGCCATGTCTGCAATCCAGGAGG
 ACAGAAGGCCAGCTCAGTGGGCCCCGCTCCCAACCCCAACGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 GAAAGTGTGTCCAGTCCGCAATTTGAGCTTGTCTGGGCCCCAGCCCAACCTGGCTGGGCTCAGTGTCTGTA
 GTTGCAGTAAAGCTATAACCTTGAATACAA

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FIGURE 64

MTTWSLRRRPPARTLGLLLLVVLGFLVLRRLDWS TLVPLRLRHRQLGLQAKGWNFMLEDSTFW
IFGGSIH YFRVPREYWRDRLLKMKACGLNTLT TYVPWNLHEPERGKFD FSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMLRRTTYKGFTEAVDLYFDHLMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVVKALEDRGIVELLTSDNKDGLSKGIVQGVLAT
INLQSTHELQLLTTFLFNVQGTQPKMVM EYWTGWFD SWGGPHNILD SSEVLKTVSAIVDAGS
SINLYMFHGGTNFGFMNGAMHFDYKSDVTSYDYDAVLTEAGDY TAKYMKLRDFFGSI SGIP
LPPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKPINMENLPVNGGNGQSFGYIILYE
TSITSSGILSGHVHDRGQVFVNTV SIGFLDYKTTKIAVPLIQGYTVLRILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYSLDMKKSFFQRFGLDKWXSLPETPTLPAPFFLGSL SIS
STPCDTPLKLEGWEKGVVFINGQNLGRYWNIGPQKTLYLPGPWLSSGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCCCAGGACC
 CTGTTGAGGGTTCTCTACTTTGGCCCTTCGGTGGGGGTCAAGACGCGAGGCACCTACGCCAAAGG
 GGAGCAAAGCCGGGCTCGGCCGAGGCCCCAGGACCTCCATCTCCCATGTTGGAGGAATC
 CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
 AAGAACTGTCTCTGCCTTCGTTCCCTGTCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
 GGCAGACACTCGGTCTGTTCTAGTGGATAGGGGTCTGACCGGTTTCTCCTAGACGGGGGCC
 CGTTCGGCTATGTGTCTGGCAGCCTGCCTACTTTCCGGGTACCGGGGTGCTTTGGGCCGAC
 CGGCTTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTTATGTGCTTGGAACTA
 CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGGACCTCATTGGCCTTTCTGA
 ATGAGGCAGCTCTAGCGAACCTGTGTGTCATCTGAGACCGAGGACCTTACATCTGTGCAGAG
 TGGGAGATGGGGGTCTCCCATCTCGTTGCTTCGAAAACCTGAAATTCATCTAAGAACCTC
 AGATCCAGACTTCTTTCGCCGAGTGGACTCCTGGTTCAAGGCTCTTGCTGCCCAAGATATATC
 CATGGCTTTATCACAATGGGGGCAACATCATTAGCATTCAAGGTGGAGAATGAATATGGTAGC
 TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGGCTCTTCCGTGCACTGCTAGG
 AGAAAAATCTTGCTCTTCACCACAGATGGGCTGAAAGGACTCAAGTGTGGCTCCCTCCGGG
 GACTCTATACCACGTGATAGTTTGGCCAGCTGACAACATGACCAAACTCTTACCCCTGCTT
 CGGAAGTATGAACCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
 CTGGGGCCAGAATCACTCCACACGGTCTGTGTGAGCTGTAAACAAAGGACTAGAGAACATGC
 TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCACTTTGGATATTGG
 AATGGTGCCGATAAAGAGGACGCTTCCTTCCGATTACTACCAGCTATGACTATGATGCACC
 TATATCTGAAGCAGGGGACCCACACCTAAGCTTTTGGCTCTTCGAGATGTCTACAGCAAGT
 TCCAGGAAGTTCTCTTTGGGACCTTTACCTCCCGGAGCCCCAAGATGATGCTTGGACCTGTG
 ACTCTGCACCTGGTTGGGCATTTTACTGGCTTTTCTAGACTTGTCTTTGCCCGGCTGGGGCCAT
 TCATTCAATCTTGCCAATGACCTTTGAGGCTGTCAAGCAGGACCATGGCTTCATGTTGTACC
 GAACCTATATGACCCATAACATTTTGGAGCCAACACCATTCTGGGTGCCAAATAATGGAGTC
 CATGACCGTGCCCTATGTGATGGTGGATGGGGTGTTCAGGGTGTGTGGAGCGAAAATATGAG
 AGACAAACTATTTTTCAGCGGGGAACTGGGGTCCAACTGGATATCTTGGTGGAGAACATGG
 GGAGGCTCAGCTTTGGGTCTAACAGCAGTGACTTCAAGGGCCTGTTGAAGCCACCAATTCTG
 GGGCAAACAATCCTTACCCAGTGGATGATGTTCCCTCTGAAAATGATAACCTTGTGAAGTG
 GTGGTTTCCCTCCAGTTGCCAAAATGGCCATATCCTCAAGCTCCTTCTGGCCCCACATTTCT
 ACTCAAACATTTCCAATTTTAGGCTCAGTTGGGGACACATTTCTATATCTACCTGGATGG
 ACCAAGGGCCAAGTCTGGATCAATGGGTTTAACTTGGGCCGCTACTGGACAAAGCAGGGGCC
 ACAACAGACCCCTACGTGCCAAGATTCTGTCTGTTTCTTAGGGGAGCCCTCAACAAATTA
 CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTTTGGATAAGCCTATC
 CTCAATAGCACTAGTACTTTGACACAGGACACATATCAATTCCTTTTCAGCTGATACACTGAG
 TGCCTCTGAACCAATGGAGTTAAGTGGGCACGAAAGGTAGGCGGGCATGGTGGCTCATGC
 CTGTAATCCAGCACTTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAGGACTTCAAGA
 CCAGCTTGCCCAACATGGTGAAACCCGCTCTCCACTCAATAAATACAAAATAGCCGGGGCTG
 ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAAATTGCTTGAATCC
 AGGAGGCAGAGGTTGTCAGTGAAGTGGAGTTGTACCAGTGCATCCAGCCTGGCTGACAGTGA
 GACACTCCATCTCAAAAAAAAAA

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FIGURE 66

MAPKKLSCLRSLLLP LSLTLLLPQADTRSFVVD RGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRL LKMRWSGLNAIQFYVPWNYHEPQPGVYNFN GSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGG LPSWLLRKPEIHLRTSDPDFLAAVD SWFKVLLPKIYPWLYHNGGNIISIQVENE
YGSYRACDFS YMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGlyTTVD FGPADNMTKIF
TL LRKYEPHG PLVNSEYYTGWLDYWGQNHSTRSVSAVTKGLENMLKLGASVNMVMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFA LRDVISKFQEVPLGPLPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTPFWVPN
NGVHDRAYVMVDGVFQGVVERNM RDKLFLTGKLGSKLDILVENMGRLSFGSNS SDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPI LGSVGDTFLYL
PGWTKGQVWINGFN LGRYWKQGPQQTLYVPRFLFP RGA LNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADTL SASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

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FIGURE 67

GCCTTTGAACACGCTCTGCAAGCCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTTATCTGCCTCTACACTCTCTTCTGGTTATTTCAGGATACCTTTGAAGGAATATT
CTTTCGAAAAAGTCAGAGAAGAGAGCAGTTTTAGTGACATTCAGATGTCAAAACGATTTTT
GCGTTCCTTCTTACATGGTAGACCAGTATGACCAGCTATATTCGAAGCGTTTTTGGTGTGTT
CTTGTGAGAAGTTAGTGAATAAATCTAGGAAATTAGTTTGAACCATGAGTGGACATTTG
AAAACTCAGGCAGCACATTTACGCAACGCCAGGACAAGCAGGAGTTGCATCTGTTTCATG
CTGTGCGGGGTGCCCCGATGCTGTCTTTGACCTCAGAGACTGGATGTGCTAAAGCTTGAAC
AATTCAGAGAAGCTAAATTCCTGCTAAGATTTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCTGCAAAAGTTGAACAGACTGCTTTTAGCTTCTTCGCGATCACTTGAGA
TGCTTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCTGCCTGGGTGTATTTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTTGAACCTGAAAAAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCGGCACCTTAAGATTCTCCACGTGAAGAGCAATTTGACCAAAGTT
CCCTCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCAGA
ACTGTGAGCTAGAGAATAATCCCATGCTATTTTCAGCCTCTCTAATTTACAGGAACTGGAT
TTAAAGTCCAATAACATTTCGCACAATTGAGGAAATCATCAGTTTCCAGCATTTAAAAACGACT
GACTTGTTTAAAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTTATTTCTTAACAACAAGCTCGAATCCTTACAGTGGCAGTATTT
AGTTTACAGAACTCAGATGCTTAGATGTGAGCTACAACAACATTTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTTGCATATCACTGGGAACAAAGTGGACATTTCTGC
CAAAACAATTGTTTAAATGCATAAAGTTGAGGACTTTGAATCTGGGACAGAAGTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGGAACTG
CTTGGAACCGCTTGCCAGCCAGCTGGGCCAGTGTGCGGATGTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTTTGATACCCTGCCACTCGAAGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCTTTGCAAAATGGGATTTAACTAAGATAATATATGCACAGTGATGTGCAGGAAC
AACTTCCTGAGTTGCAAGTGCTCAGGTACAAGTTATTACAAGATAATGCATTTTAGGAGTAG
ATACATCTTTTAAATAAAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTTGTAGGGTTTTAAGTCATTCAATTTCCAAATCATTTTCTTTTCTTTTGGG
AAAGGGAAGGAAAAATTATAATCACTAATCTTGTTCTTTTAAATGTTTGTAACTTGGAT
GCTGCCGCTACTGAATGTTTACAAATTGCTTGCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAAAAA

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FIGURE 68

MAYMLKLLISYISIIICVYGFICLYTLFWLFRIPLKEYSFEKVRRESSFSIDIPDVKNDF AFL
LHMVDQYDQLYSKRFGVFLSEVSENKLR EISLNHEWTFEKL RQHISR NAQDKQELHLFMLS G
VPDAVFDLTDL DLVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNL NSENNKMIGLESRLRLHLKILHVKS NLTKVPSN
ITDVAPHLTKLVIHNDG TKLLVLNSLKKMMNVAELELQNC ELERIPHAIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLES LYFSNNKLES LPVAVFSLO
KLRC LDVSYNNISMIP IEIGLLQNLQHLHITGNKV DILPKQLFKCIKRLTNLGGNCITS LP
EKVGQLS QLTQLELKGNC LDR LPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

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FIGURE 69

CCCACGCGTCCGGCCTTCTCTCGGACTTTGCATTTCATTCTCTTTTCATTGACAACTGACTTTTTTTATTTCT
 TTTTTCCTATCTCTGGGCGAGCTTGGGATCCTTAGGC CGCCCTGGGAAGACATTGTGTGTTTACACACATAAGGAT
 CTGTGTTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCAITGCTTAGTGGTTGTGTGGGAGGGAGACACGTGG
 GCTCAGTGGTCTGCTTGCACTTATCTGCCCTAGGTACATCGAAGTCTTTTGACCTCCATACAGTGATTATGCGCTGTC
 ATCGCTGGTGGTATCCCTGGCGGCTTGTCTCTGTGATAGTTGTCTGTCTCTGTCTTTACTTCAAAATACACAAC
 GCGCTAAAGCTGCAAGAGAACTGAAGCTGTGGCTGTAAATAACACAACCCAGACAGGTGTGGTGGGCGAAG
 AACAGCCAGGCCAAAACCAATTGCCACGGAGTCTTGTCTGCCCTGCAGTGTGTGAAGGATATAGAATGTGTGCC
 AGTTTGTATTCCCTGCCACCTTGTCTGTGCGACATAAATGAGGGCTCTGAGTTAGGAAGGGCTCCCTTCTCAAA
 GCAGAGCCCTGAAGACTTCAATGATGTCAATGAGGCCACTGTGTTGTGATGTGCAGGCCACAGAAGAAAGGCCACAG
 CTCGCCATCAGTTTCAATGAAAAATACTCAGTGCCTGCTGGGAACACAGTGTGTGAGAGATCCCTACAGAGAGCTTC
 CACTGGGGGCAACCCCTCCAGGAAGGAGTTGGGGAGAGAGAACCTCACTGTGGGGAATGCTGATAAAACCATCA
 CACAGCTGCTCTATTCTCACACAAATCTACCCCTTGGCTGGCTGGAACCTGACGTTTCCCTGGAGGTGTCCAGAAA
 GCTGATGTAAACACAGAGCCTATAAAAGCTGTGCGTCTTAAGGCTGCCAGCGCCCTGCCAAAATGGAGCTTGTA
 AGAAGGCTCATGCCATTGACCCCTCTTAATTCTCTCTGTTTGGCGGAGCTGACAAATGGCGGAGGCTGAAGGCAAT
 GCAAGCTGCACAGTCACTGATAGGGGGTGCCCAATATGGCAGAGACCCAACAAGCCATGATCTTGCAACTCAATCCC
 AGTGAGAACTGCACCTGGACAATAGAAAACAGAAAAACAAGCATCAGAATTATCTTTTCTATGTCCAGCTT
 GATCCAGATGGAAGCTGTGAAAGTGAAAAACATAAAGTCTTTGACGGAACCTCCAGCAATGGGCTCTGCTAGGG
 CAAGTCTGCAGTAAAAACGACTATGTCTCTGTATTGTAATCATCATCCAGTACATTGACGTTTCAATAGTTACT
 GACTCAGCAAGAATTCAAAGAACTGTCTTTGTCTTCTACTACTTCTTCTCTCTCAACATCTCTATTCCAAACTGT
 GCGCTGTGCTCCTGGATCAAGTTGGGAAGATCTCTCACCGACCCCAATTACCCAAAGCCGATCTTGAGCTGGCTGT
 TGTGTGTAGGACATACAGTGGAGAAAGATTACAAGATAAACTAAACTCAAGAAGATTCTCTAGAAATAGAC
 AAAACGTGCAAAATTTGATTTTCTGCCATCTATGATGCGCCCTCCACCAACTCTGGCCTGATGGACAAGTCTGT
 GCGCGTGTGACTCCCACTCTCGAATCGTCACTCAAACTCTGACTGTGCTGTGTCTACAGATTATGCACTTCT
 TACCGGGGATTTTCTGCTCTCTCACTCAATTTATGCAGAAAACATCAACATACATCTTTAACTTGTCTCTCT
 GACAGCTGACAGTCACTTATTAAGCAATCTCACTAGAGGCTTTTAACTTAATGGGAATAACTGCAACTAAAA
 GACCCAACCTTGCAGACCAAAATTAATCAAAATGTTGTGGAATTTCTGTCTCTCTTAATAGGATGTGGTACATCAGA
 AAGGTAGAAGATCACTCAATTACTACACCAATATAATCACTTTTCTGATCTCAACTCAAGATTCGAAGTGATCACC
 CGTCAGAAACAACCTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
 GAAGATGATGTAATACAAAGTCAAAATGCACTGGGCAAAATATACACAGCATGGCTCTTTTGAATCCAAATCA
 TTTGAAAAGACTATACTTGAATCACCATATTATGTGGATTGGAACCAAACTCTTTTGTGTCAAGTTAGTCTGCAC
 ACCTCAGATCCAAATTTGGTGGTGTCTTGTATACCTGTAGAGCCTCTCCCACTCTGACTTTGCTATCTCCACCC
 TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGAAGGTGATCCCTTATTTTGGACACTATGGGAGA
 TTTCAAGTTAATGCTCTTAAATCTCTGAGAAGTATGAGCTCTGTGATCTGCACTGTGAAAGTTTGTGATGTGAT
 AGCAGTGACCCAGCTCTCGCTGCAATCAAGGTGTGTCTCCAGAAGCAAAACGAGACATTTCTCATATAAATGG
 AAAACAGATTCCATCATAGGACCAATTCGTCTGAAAGGGGATCGAAGTGAAGTGGCAATTCCAGGATTTCAAGAT
 GAAACAATGCGGGAAGAACTCCAAACCAAGCTTTCAACAGTGTGATCTTCTTCTCATGTTCTAGCTCTG
 AATGTGTGACTGTAGCGCAATACAGTGAAGGCAATTTGTAAATCAACGGGACAGACTCAAAATACAGAGGCTG
 CAGAACTATTAACTAACAGGTCCAACTTAAGTGAACATGTTTCTCCAGGATGCGAAGGAAATGCTACCTCGT
 GCCTACACATATTATGAATAAATGAGGAAGGGCTTGAAAGTGACACACAGGCTGCATGTAAAAAAA

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Signal sequence:

Transmembrane domain:

N-glycosylation site.

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAGAACAGCGCTCCCAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCCAGGCTCGCGTTCCCGTTGCTGCTGTTGCTGCTG
TGCTGCCGCCGCCGCGTGCCTGCCACAGCGCCAGCGGTTTCGACCCCACTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTTGACAGGCCAAGTTCGGCATCTTCATCCACTG
GGGAGTGTTCCTGTCGCCAGCTTCGGTAGCGAGTGGTTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGGAATTTATGAAAGATAATTACCTCCTAGTTTCAAATATGAAGAT
TTTGGACCACTATTTACAGCAAAATTTTTTAATGCCAACCAAGTGGGCAGATATTTTTCAGGC
CTCTGGTGCCAAATACATTGCTTAACTTCCAAACATCATGAAGGCTTTACCTTGTGGGGT
CAGAATATTTCGTGGAATGGAAATGCCATAGATGAGGGGCCAAAGAGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTCGCTTTTGGACTGTACTATTCCTTTTGA
ATGGTTTCATCCGCTCTTCTTGAGGATGAATCCAGTTTCATCCATAAGCGGCAATTTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGTTGACGGAGGAGCACCGGATCAATACTGGAAACAGCACAGGCTTCTTGGCCTGGT
ATATAATGAAAGCCAGTTCGGGGCAAGTATGACAGTACCAATGATCGTTGGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTATACCTGCACTGATCGTTATAACCCAGGACATCTTTTGCCA
CATAAATGGGAAAACATGCATGACATAGACAACTGCTCTGGGGCTATAGGAGGGAAGCTGG
AATCTCTGACTATCTTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTTCATGTG
GAGGAAATCTTTTGATGAATATGGGCCCCACATAGATGGCACCATTCTGTAGTTTTTGAG
GAGCGACTGAGGCAAGTGGGGTCTTGGCTAAAAGTCAATGGAGAAGCTATTTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCAACCCAGATGTGTGGTACACATCCAAAGCCTAAAG
AAAAATTAGTCTATGCCATTTTCTTAAATGGGCCACATCAGGACAGCTGTTCCTTGGCCAT
CCCAAAGCTATTCTGGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACTG
GATTTCCTTTGGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCAATTCATCAGATGC
CGTGTAAATGGGGCTGGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCATATGGAGA
AAGCAATGTAACTGGATAAGAAAATTTATTTGGCAGTTTCCGCTTTTCCCACATA
AATTTTTCTTAAATTACCATGTAAACATTTTAACTCTCCAGTGCATTTGCCATTAAGTCT
TCTTCACATTGATTTGTTTCCATGTGTGACTCAGAGGTGAGAATTTTTTACATTATAGTAG
CAAGGAATTTGGTGTATTATGGACCGAACTGAAAATTTTATGTTGAAGCCATATCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGGATATTTCTGGGAAATGCATTGTAGTCAAT
TTTTTTTTTGTGCCAACATCATAGAGTGTATTTACAAAATCCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCCTAGGCTACAGACATATACAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAACATAGAGAAG
GTACAGTAAAAATACTGTAAATAAATGGTGCACCTGTATAGGGCACTTACCAGGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCTTAGGACATTA
TTGAACACTGCCAGCGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTTCTTTCTTCAATTATAAATAACATAAGTGTACTGTAACCTTACAAACGTTTTTAAT
TTTAAACCTTTTGGCTCTTTGTATAAACACTGACTTAAACATAAACTCATTGTGCAA
ATGTAA

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FIGURE 72

MRPQELPRLAFPLLLLLLLLLPPPPCPAHSATRFDPWTESLDARQLPAWFDQAKFGIFIHWG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPSPFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHHEGFTLWGSEYSWNWNAIDEGPKRDIVKEVAIRNRTDLRFGLYYSLEFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVINDRWAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIBELVKQLVETVSCGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDIVTPDVWYTSKPKKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHGQPLNWI
SLEQNGIMVELPQLTIHQMPCKKGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

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FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTCAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAGTGGCCATC
TGAGGTGTTTCCCTGGCTCTGAAGGGGTAGGCACGATGGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTTCCATCTGGACCACGAGGCTCTGGTCCAAGGCTCTTTGCGTGCAGAAGAGCT
TTCCATCCAGGTGTCTATGCAGAAATTATGGGGATCACCTTGTGAGCAAAAAGGCGAACAGC
AGCTGAATTTACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTTGAAAGCTAGCTTTGAAACTTGCAGCTATGGCTGGGTGGAGA
TGGATTGCTGGTCATCTCTAGGATTAGCCCAAAACCCCAAGTGTGGGAAAAATGGGGTGGTG
TCCTGATTTGGAAGGTTCCAGTGAAGCCGACAGTTTGCAGCCTATTGTTACAACCTCATCTGAT
ACTTGGACTAACTCGTGCATTCCAGAAATTATCACCACCAAAGATCCCATAATTCAACACTCA
AACTGCAACACAAACACAGAATTTATTGTCTAGTGACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACTTGGCCCTACTACTACTCTCTCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTACAGAAAGTTTATGGAAGTCTAGCACCATGTCTACAGAAAC
TGAACCATTTGTGAAAAATAAGCAGCATTCAAGAAATGAAGCTGCTGGGTTTGGAGGTGTC
CCACGGCTCTGCTAGTGCTTCTCTCTCTTCTTGGTGTCTGCAGTGGTCTTGGATTTTGC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTTTACAAACAAGAATCAGCAGAAGGAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAAGGCCAATGATAGCAACCCTAATGAGGAATCAAAGA
AACTGATAAAAAACCAGAGAGTCCAAGAGTCCAAGCAAACTACCGTGCATGTCTGGAA
GCTGAAGTTTAGATGAGACAGAAAATGAGGAGACACACCTGAGGCTGGTTTCTTCATGCTCC
TTACCCCTGCCAGCTGGGGAAATCAAAGGGCCAAAGAACCAAAGAAGAAAGTCCACCTT
GGTTCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAGAGAATGC
CCTTCTCCTTATTGTAAACCTGTCTGGATCCTATCCTCCTACCTCAAAGCTTCCACGGCC
TTTCTAGCCTGGCTATGTCTTAATAATATCCCACTGGGAGAAAGGAGTTTTCGAAAGTGCAA
GGACCTAAAACATCTCATCAGTATCCAGTGGTAAAGGCCTCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGACCAAGGCTTCTCTACTGATTCCGAGCTCAGAC
CCTTCTCTCAGCTCTGAAAGAGAAACAGTATCCCACCTGACATGTCTCTGAGCCCGTA
AGAGCAAAAGAAATGGCAGAAAAGTTTAGCCCTGAAAGCCATGGAGATTCTATAACTTGAG
ACCTAATCTCTGTAAAGCTAAAATAAGAAATAGAACAAAGGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAAACACAGACAGGGTCAAAGTGTCTCTGAAACACATTGAGTTGGA
ATCACTGTTTGAACACACACACTTACTTTTCTGGTCTCTACCCTGCTGATATTTTCTCT
AGGAAATATACTTTTACAAGTAACAAAATAAAAACTCTTATAAATTTCTATTTTATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTTGTTAAAAAGTAATAAAATTA
ACAAACATTTGCTGAATAGCTACTATATGTCAAGTGTCTGTGAAGGTATTACACTCTGTAAT
TGAATATTATCTCTCAAAAATTGACATAGTAGAACGCTATCTGGGAAGCTATTTTTCATCA
GTTTGTGATATTTCTAGCTTATCTACTTCCAAACTAATTTTATTTTGTCTGAGACTAATCTT
ATTCAATTTCTCTAATATGCAACCATTTATAACCTTAATTTATTATTAACATACCTAAGAAG
TACATTTGTTACCTCTATATACCAAGCACATTTTAAAGTGCCATTAAACAAATGTATCACTA
GCCCTCTTTTCCAAACGAAGGAGCTGAGAGATGCAAAATATTTGTGACAAAAAATTAA
AGCATTTAGAAACTT

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FIGURE 74

MARCFSLVLLLTISIWTRRLVQGSRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVVGDGFVVISRISPNPKCGKNGVGLIWKVPVSRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKAAFKEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFNTKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

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FIGURE 75

AGATGCGGCTCTTGGCACCTCTAATTGCTCTCGTGTATTTCGGTGCCGCGACTTTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTGCGCCCTGCTCTCTGCTGCCCTTCTACTCTGTGAGGAA
ACTGCCGCCGCTCTGCCACGCTCTGCCACCCCAACGCGAAGACGGTAACCCGTGTGACTTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTTCATGTTTGTAGTAAAGTGCCCAACACAAT
TCTTTTCTTCCGCTTGGATATTTCGCATGGGCCTACTTTACATCACACTCTGCATAGTGTTC
TGATGACGTGCAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGGACAAGAGGGTCACCTTGGATTGTGGAGTTCTTTGCCAA
TTGGTCTAATGACTGCCAATCATTTGCCCTATCTATGCTGACCTCTCCCTTAAATACAACT
GTACAGGGCTAAATTTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGCGGTAC
AAAGTGAGCATCACCCCTCACCAGCAACTCCCTACCTGATCCTGTTTCCAAGGTGGCAA
GGAGGCAATGCGGCGGCCACAGATTGACAAGAAAGGACGGGCTGTCTCATGGACCTTCTCTG
AGGAGAATGTGATCCGAGAATTTAACTTAAATGAGCTATACCAGCGGGCCAAGAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTTCAACCCCCACCACAGTGTGAGA
TGGGGAAAACAAGAAGGATAAAATAAGATCCTCACTTTGGCAGTGCTTCTCTCTGTCAATT
CCAGGCTCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTTNATNATGTTTTCCCTTTGG
CTGNGACTGGNTGGGGCAGCATGCAGCTTCTGATTTTAAAGAGGCATCTAGGGAATTGTCAG
GCACCTTACAGGAAGGCCTGCCATGCTGTGGCCAACTGTTTCACTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGGAAATGGTTTCCCTCCAAGCTTGGGTCACTGTGTTAACTGCTTATC
AGCTATTGAGACATCTCCATGGTTTCTCCATGAAACTCTGTGGTTTCATCATTCCTTCTTAG
TTGACCTGCACAGCTTGTTAGACCTAGATTTAACCCCTAAGGTAAGATGCTGGGGTATAGAA
CGCTAAGAAATTTTCCCCAAGGACTCTTGCTTCCTTAAAGCCCTTCTGGCTTCGTTTATGGTC
TTCATTAAAGTATAAGCCTAACTTTGTGCTAGTCTCTAAGGAGAAACCTTTAACCCAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTTGTGGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTTCCTTTGTGTGGTAGGACTTGGAGGAGAAATCCCTGGACTTTCAC
TAACCTCTTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAAGATTGGGATT
TCCTTTTG

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FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPPYYLLSALLSAAFLLVKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFPAPIYADLSLKYN
TGLNFGKVDVGRYTDVSTRYKVSTSP LTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

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FIGURE 77

GGACAGCTCGCGGCCCCGAGAGCTCTAGCCGTCGAGGAGCTGCCTGGGGACGTTTGCCCTG
GGGCCCCAGCCTGGCCCGGTACCCCTGGCATGAGGAGATGGGCCCTGTTGCTCCTGTTCCCA
TTGCTCCTGCTGCCCGCTCCTACGGA CTGCCCTTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCATGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGCGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGGCGTTACCGCTGTGAGGTCATTGACGGGCTGGA
GGATGAAAGCGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGTCTTTCCCTTACCAAGTCCCCCA
ACGGGCGCTACCAAGTCAACTTCCACGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTTGAGCAGCTCTTCCGGGCTTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCGAGCCCTGCGGTGGCC
CAGGCTTGGCAGCTGGCGTGCAGAGCTACGGCCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCTGCCAGGAAGATGATGCCACGATCGCCAAGGTGGGAC
AGCTCTTTGCGCCCTGGAAGTTCATGGCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCTGTGGTTCACCCGCATCCTAACTGTGGGCCCCAGAGCCTGGGGT
CCGAAGCTTTGGCTTCCCGACCCGAGAGCCGCTTGACGGTGTTTACTGCTACCGCCAGC
ACTAGGACCTGGGGCCCTCCCTGCGCATTCCTCACTGGCTGTGATTTATTGAGTGGTT
CGTTTTCCCTTGTGGGTGGAGCCATTTAACTGTTTTTATACTTCTCAATTTAAATTTTCT
TTAAACATTTTTTTACTATTTTTGTAAAGCAACAGAACCCAAATGCCTCCCTTTGCTCCTG
GATGCCCCACTCCAGGAATCATGCTTGCTCCCTGGGCCATTTGCGGTTTTGTGGGCTTCTG
GAGGGTTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGGC
GGTGGCTGTCTAGAATGCCGCGGGAGTCCGGGCATGGTGGGCACAGTTCTCCCTGCCCTT
CAGCCTGGGGGAAGAAGAGGGCCTCGGGGGCTCCGGAGCTGGGCTTTGGGGCTCTCTGCC
CACCTCTACTTCTCTGTGAAGCCGCTGACCCAGTCTGCCCACTGAGGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTTCCAGCGAAATCTGAGGGAAGGAAGAACTCCCCCTCCCGTTCCCTT
TCCCTCTCGGTTCCAAAGAATCTGTTTTGTGTGTCATTTGTTTCTCTGCTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTGACTTTGGACAATAAATGGTGTCTGACTGCTTCCGTCGCA
AA
AA

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FIGURE 78

MGLLLLVLPLLLPGSYGLPFYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFQELFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGPR
HRRRLHRYDVFCFATALKGRVYYLEHPEKLTLEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

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FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCGATGATGTGGCGACCATCAGTTCGTCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGGCCCCCTGAGCGACGCTCCCATGATGACGCCACGGGAA
CTTCCAGTACGACCATGAGGCTTTCTTGGGACGGGAAGTGGCCAAGGAATTCGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGCTCTGGGGCGGATCGTGGACCGCATGGACCGCGCGGGGGAC
GGCGACGGCTGGGTGTCTGCTGGCCGAGCTTCGCGCGTGGATCGCGCACACGCAGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCCTGGGACACGTACGACACGACCGCGACGGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGGCCACTACGCGCCCGTGAAGAATTTTCATGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGGACGAGCGCGTTCCTCGGGTGGC
CGACCAGGATGGGGACTCGATGGCCACTCGAGAGGAGCTGACAGCCTTCCTGCACCCCGAGG
AGTTCCCTCACATGCGGGACATCGTGATTGCTGAAACCTCGGAGGACCTGGACAGAAAAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGAGTTCGGGACTTCGGGATCTGAACAAGG
ATGGGCACCTGGATGGGAGTGAGGTGGGCCACTGGGTGCTGCCCCCTGCCAGGACCAAGCCC
CTGGTGAAGCCAAACCTGCTGCACGAGAGCGACACGGACAAGGATGGGCGGCTGAGCAA
AGCGGAAATCTGGGTAATTGGAACATGTTTGTGGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCACGATGAGCTGTGAGCACC CGCACCTGCCACAGCCTCAGAGGCCCG
CACAAATGACCGAGGAGGGGCGCTGTGGTCTGGCCCCCTCCCTGTCCAGGCCCCGAGGAG
GCAGATGCAGTCCCAGGCATCCTCCTGCCCCTGGGCTCTCAGGGACCCCCCTGGGTGCGCTTC
TGTCCTGTACACCCCCAACCCAGGGAGGGGCTGTATAGTCCAGAGGATAAGCAATAC
CTATTTCTGACTGAGTCTCCAGCCAGACCCAGGGACCTTGGCCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCCAAATCTGAGCCTCCACCACATAGACTGAAACTCCCTT
GGCCCCAGCCCTCTCCTGCTGGCCTGGCCTGGGACACCTCTCTGCCAGGAGGCAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

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FIGURE 80

MMWRPSVLLLLLLLRHGAQGKPSDAGPHGQGRVHQAAPLSDAPHDDAHGNFYDHEAFLGR
EVAKFEDQLTPESQARLGRIVDRMDRAGDGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTRDRGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQGDGSMATRE
ELTAFLHPPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPANVQTERQQ
FRDFRDLNKDGHLDGSEVGHWVLPAPQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

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FIGURE 81

GGGGCCTTGCCCTTCGCCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCGGGCGGGGTGCGAGGGGATCCCTGACGCCCTCTGTCCCTGTTTCTTTGTCTGCTCCCG
CCTGTCTGTCTGTCGTTTGGCGCCCCCGCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTTCGCCGCCGAGGCGCCTCCAGACCTAGAGGGGGCGCTGGCCCTGGAGCAG
CGGGTCGTCTGTGTCCTCTCTCCTCTGCGCCGCGCCCGGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACGCGCGGGGCCCTCCCGCACCTTGGCCTTGCCCGCATTTCTCCTCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCGCGGGGCCCGCGGGCAGCGAGGGAGCCGCTCCCATTTGCTATCACATG
TTTTACCAGAGGCTTGGACATCAGGAAAGAGAAAGCAGATGTCCTCTGCCCAGGGGGCTGCC
CTCTTGAGGAATTTCTCTGTGTATGGGAACATAGTATATGCTTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGGATTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACTATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAAATGCTTTCTAGAT
GGTCTGCTTTCTTACAGTAACAAAGGCCAAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGAGCTAAAGAAAAACCCGAGAAGAAAACTGG
CAATAAAGATTGTAAGCAGACATTGCATTCTCTGATTGATGGAAGCTTTAATATTGGGCAGC
GCCGATTTAATTACAGAAGAAATTTGTTGGAAAAAGTGGCTCTAATGTTGGGAATTGGAACA
GAAGGACCATATGTGGGCCTTGTTCAGGCCAGTGAAATCCCAAAATAGAATTTACTTTGAA
AAACTTTACATCAGCCAAAGATGTTTTGTTTGGCCATAAAGGAAGTAGGTTTCAGAGGGGGTA
ATTCGAATACAGGAAAAAGCCTTGAAGCATACTGCTCAGAAATTTCTTCCAGGTAGATGCTGGA
GTAAGAAAAAGGATCCCAAGTGGTGGTGGTATTTATGATGGTTGGCCTTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTTGGTGTCAATGTATTATAGTTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGGATGGTTCAGGATGTCAATTTGTTGACAAGGCTGTCTGT
CGGAATAATGGCTTCTTCTCTTACCACATGCCCAACTGGTTTGGCACCACAAAATACGTAA
GCCTCTGGTACAGAAGCTGTGCACCTCATGAACAAATGATGTGCAGCAAGACCTGTTATAACT
CAGTGAACATTGCTTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTTCCGCCTC
ATGCTTGAATTTGTTTCCAACATAGCCAAGACTTTTGAATCTCGGACATTTGGTGCCAAGAT
AGCTGCTGTACAGTTTACTTTATGATCAGCGCAGCGAGTTTCACTTTCACTGACTATAGCACC
AAGAGAATGTCTAGCTGTCTATCAGAAACATCCGCTATATGAGTGGTGGAAACAGCTACTGGT
GATGCCATTTCCCTTCACTGTTAGAAATGTGTTTGGCCCTATAAGGGAGAGCCCCAACAAAGAA
CTTCTAGTAATTGTGCAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACATCTTCTCTGTTGGTGTGGCTTGGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTCTCACAAGAGAGTTACAGGATT
AGAACCAATTGTTTCTGATGTCTATCAGAGGCATTGTAGAGATTTCTTAGAATCCCGACAAT
AATGGTAACATTTTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTTGTATT
CTCATAAATCAGAAATGCTTTAGCATACTAGAAATCAGATACAAAATTAAGTATGTCAAC
AGCCATTTAGGCAAATAAGCACTCCTTTAAAGCCGCTGCGCTTCTGGTTACAATTTACAGTGT
ACTTTGTTAAAAACACTGCTGAGGCTTCAATAATCATGGCTCTTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAACCTTAAAGAGTTTCAACCATGCCTACTAAATGTACAGATATGCAAA
TTCCATAGCTCAATAAAGAAATCTGATACTTAGACCAAAAAAAAAA

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FIGURE 82

MSAAWIPALGLGVCLLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPPGGCPLEEFVSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIGQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAlKEVGRGGNSNTGKAL
KHTAQKFFTVDAQVRKGIPKVVVVVFIDGWPSDDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNI AFLI
DGSSSVGDSNFRMLLEFVSNI AKTFRISDIGAKIAAVQFTYDQRT EFSFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

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FIGURE 83

CGCCGCGCTCCCGCACCCGCGGCCGCCACCGCGCGCTCCCGCATCTGCACCCGAGCCCG
GGCGGCTCCCGCGGGAGCGAGCAGATCCAGTCCGGCCCCGAGCGCAACTCGGTCCAGTCG
GGCGGCGGCTGCGGGCGCAGAGCGGAGATGCGAGCGGCTTGGGGCCACCCTGCTGTGCTGCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCCGGCCCGGCTCTCAGTACCCGAGGAGGAGGCCACCCCTCAATGAGATGTTCCGCGA
GGTTGAGGAATGATGGAGGACACGACGACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACCTTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGGAATAATACCATCCATGTGCACCCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTTCAGAGACAGTTATCATCATCTG
TGGGAGACGAAGAAGGCAGAGGAGGCCAGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTACTGCCAGTTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGTGTGTGTCTGGGGTCACTGCACCAAAA
TGGCCACCAAGGGGACAGCAATGGGACCATCTGTGACAAACAGAGGGAAGTCCAGCCGGGGCTG
TGCTGTGCTTCCAGAGAGGCTGCTGTTCCCTGTGTGTCACACCCCTGCCCGTGGAGGGCGA
GCTTTGCCATGACCCCGCCAGCCGGCTTCTGGACCTCATCACCTGGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCTCCTCTGCCAGCCCCAGAGCCACAGCCCTG
GTGTATGTGTGCAAGCCGACCTTCGTGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCTCCGATGAGTATGAAGTTGGCAGCTTCATGGAGGAGGTGCGCCAGGAGCTGG
AGGACCTGGAGAGGAGCTGACTGAAGAGATGGCGCTGGGGAGCCTGCGGCTGCCGCCGCT
GCACTGCTGGGAGGGGAAGAGATTAGACTCTGGACCAGGCTGTGGGTAGATGTGCAATAGAA
ATAGCTAATTTATTTCCCGAGGTGTGTGCTTTAGGCGTGGGCTGACAGGCTTCTTCTTACA
TCTTCTTCCAGTAAGTTTCCCTCTGGCTTGACAGCATGAGGTGTTGTGCAATTTGTTACG
TCCCCAGGCTGTTCTCCAGGCTTCACAGTCTGGTGCTTGGGAGAGTCAGGCAGGGTTAAAC
TGCAGGAGCAGTTTGCCACCCCTGTCCAGATTATTGGTGCTTTGCTCTACCAAGTTGGCAG
ACAGCCGTTTGTCTACATGGCTTTGATAATTGTTTGGGGGAGGAGATGGAACAATGTGG
AGTCTCCCTCTGATTGGTTTTGGGGAATGTGGAGAAGAGTGCCTGCTTTGCAACATCAA
CCTGGCAAAAATGCAACAAATGAATTTTCCACGCAAGTCTTTCATGGGCATAGGTAAGCTG
TGCTTCAGCTGTTGCAGATGAAATGTTCTGTTACCCCTGCATTACATGTGTTTATTCTCC
AGCAGTGTGTCTCAGCTCCTACCTCTGTGCCAGGGCAGCATTTTCATATCCAAGATCAATTC
CCTCTCTCAGCACAGCTGGGGAGGGGGTCAATGTTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCCAAGTCAACAGCTAGTGAAGACCAGAGCAGTTTCAT
CTGGTTGTGACTCTAAGCTCAGTGCTCTCTCCACTACCCCAACCAGCCTTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAAG
GTCAAACTAATTTCTACATCCCTCTAAAAGTAACTACTGTTAGGAACAGCAGTGTTCTCAC
AGTGTGGGGCAGCGCTCCTTCTAATGAAGACAATGATATTGACATGCTCCTCTTGGCAGT
TGCATTAGTAACTTTGAAAGGTATATGACTGAGCGTAGCATACAGGTTAACTGCAGAAACA
GTACTTAGGTAATTTAGGGCGAGGATTATAAATGAAATTTGCAAAATCACTTAGCAGCAAC
TGAAGACAATATCAACACAGCTGGAGAAAAATCAACCGAGCAGGGCTGTGTGGAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAATGATGTTTTCAGGTGTCA
TGGACTGTTGGCCACCATGTTTTCATCCAGAGTTCCTAAAGTTTAAAGTTGCACATGATTGTA
TAAGCATGCTTTCTTTGAGTTTTAAATTATGTATAAACATAAGTTCATTAGAAATCAAGC
ATAAATCACTTCACTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAAASSEVNLANLPSPYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRQQRMLCTRDSECCG
DQLCVWGHCTKMATRGSGTICDNQRDCQPGGCCAFQGRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPCASGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEV
GSFMEEVRQELEDLERSLTEEMALGEPAAAAAALLGGEET

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

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FIGURE 85

AAGGAGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTTCAGGCCATCACTCTCCTTCCCTCCAAACACACATGTCATCTGTACACACACATACA
CACACATACACCTTCTCTCTCTCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCATAGAAAAGGACAC
TAAAGCCTTAAGGACAGGCCCTGGCCATTACCTCTGCAGCTCTCTTGGCTTGTGTAGTCAAAAACATGGGAGGGG
CCAGGCACGGTGACTACACCTTAATCCCAGCATTTTGGAGACCAGGTTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACACAGCTGGCCCAACTGGAGAAACCCCATCTCTACTAAAAATACAAAATTAGCCAGGAGTTGGTGGC
AGGTGCCCTGTAAATCCCAGCTA CT CAGGTGGCTGAGCCAGGAGATCGTTGAATCCAGGAGGCGGAGGATGCAGT
CAGCTGAAGTGCACCCGCTGCACTCCAGCTGGGTGACAGAATGAGACTCTGTCTCAAAACAAACAAACCGGAGGA
GGGGTAGATACTGCTTCTCTGCAACCTCCTTAACCTGTGACTCTCTTCTTCAGGGCTGCCCTGATGGGGCTG
GCAATGACTGAGCAGGCCCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAGTGAACGCCCG
GTGTAGAACTGACTGCCCTGGGAGGGTGGTTCTTGGGCCCTGGCAGGGTGTCTGACCCCTTACCTTGCAAAAACACA
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCTGCCCTGCAGCTCCACCATGAGGCTTCTCGTGGCCCC
ACTCTTGTAGCTTGGGTGGCTGGTCCACTGCCACTGTGCCCGTGGTACCCCTGGCATGTCCCTGCCCCCTCA
GTGTGCCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTTACCCTGAGGGCTACCACTGTGGACTGCAATGA
CCTATTCTTGACGGCAGTCCCCCGGCCACTCCCGCAGGCACACAGACCTGCTCTGCAAGAGCAACAGCAATTCG
CCGTGTGGACAGGAGTGGCTGGGCTCACTGGCCAACTCTCAGAGAGTGGACTGTCTCCAGAAACAGCTTTTGGGA
TGCCCGAGCTGTGATTTGACCTGCCCTGCCAGCTGTCTGAGCTGCACTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACCACTTTTGCAAGGCTGGCCAGCCTACAGGAACCTCTATCAACCAACCAACAGCTCTACCGCATCGC
CCCCAGGGCTTTTCTGGCCTCAGCAACTGTCTGGCTGCACTCAACTCAACTCACTCTTGAGGGGCTATGACAT
CCGCTGGTTTGAATGCTGCCAACTTGGAGATACTCATGATTGGCGGCAACAGGTAGATGCATCTCTGCAGAT
GAACCTCCGGGCCCTGGCCAACTTGGCTAGCCTGGTGTGCTAGCAGGCATGAACCTGGCGGAGATCTCCGCAATGCTG
CCTGGAGGGGCTGCAAGGCTGGAGAGCCTCTCCTTCTATGACAAACAGCTGGCCCGGCTGCCACAGCGGGCACT
GGAAACAGGTGCCCGGGCTCAAGTTCTAGACCTCAACAGAACCCGCTCCAGCGGCTAGGSCCGGGGACCTTTGG
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACAACATGAGGAGCTGGTCTCCATCGACAAGTTTGGCTTGGT
GAACCTCCCCGAGCTGACCAAGCTGGACATCAACATAAACCCACGCTGTCTCTTCACTCACCCCGCGCTCTCCA
CCACTGCCCCAGATGGAGAGCTCATGCTCAACAAACAAACGCTCTCAGTGCTTGCACACAGACAGCTGGAGTC
CTGCTCCCAACTGCGAGGAGGTAGTTCTCCAGGCCAACCCCATCCGCTGTGACTGTGTCTCATCCGCTGGGCCAATGC
CACGGGCACCCGTGTCCGCTTCTCAGAGCCGCAATCCACCTGTGTGTCGGAGCCTCCGAGCTTGGGCGCTCCG
GGTCTGAGGTGCCCTTCAGGCTGAGGAGTACGAGCACTGTTTGGCCCTCATCTCCCCAGGAAGCTTCCCCCAAG
CCTCCAGGTGAGCAGTGGAGAGGAGCATGCTGCTGCAATTGCCGGCACTGGCCGAAACCCGAGATCTACTG
GGTCACTCAGCTGGGCTTCGACTGCACTGCAACCTGCCATGCAAGTGGCTTCTGATGCCCCACACCA
GGAGCTGCGGAGGTGACAGCAGAAAGAGCCAGGCTGCCATGCGAGCAGGAGGTACCGGGTGTACCCGAGGGGACCTT
TAAGACGTTAGTGTGGTTTGGGCTGCTCTCTCCAGCAGGCGAGGACAGAGGACAGGGGCTGGAGCTCGG
GGTCAGGAGACACCCCTATCACTCTGCTATCTTGGTCAACCACCCAAACAGTGTCCACCAACCTCAC
CTGGTCACTGCTCTCTCTCCGCGGCCAGGGGGCCACAGCTCTGGCCCGCTGCTCTGGGGAACCCACAGCTA
CAACATTAACCGCTCTCTTCAAGCCAGGAGTACTGGGCTGCTCTGCAAGTGGCTTCTGATGCCCCACACCA
TTTGGCTTGTGATGGCCAGGACCAAGAGGCCACTTCTTGCCACAGAGCCTTAGGGGATGCTCTGGGCTCAT
TGCCACTCTGCTCTGCTGCTCTCTCTTGGCAGCTGGGCTAGCGGCCACTTGGCAGAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGCGGCTCTCTCTCAGCCTGGGCTTCTGGGGCTGGAGTCCCCCTTCTGTCCGGGTGTG
GTCTGCTCCCCCTGCTGCCCTGGAATCCAGGAGGAGGAGCTGCCAGATCTCTAGAAAGGGGAGACATGTTGGC
ACCATGTCTCAAAATCTTGAAGCTCAGCCTGTCTCTCAGCAGTAGAGAAATCACTAGGACTACTTTTTACAAA
AGAGAGCAGTCTGGGCCAGATGCCCCGTCAGGAAAGGGACATGGACCCACGCTGTCTGAGGCTGGCAGCTGGG
CAGACAGATGGGGCTTGTGGCCCTGGGGGTGCTTCTGCAGCCTTGAAAAAGTTGGCCTTACCTCTTAGGTC
CCTCTGCTGCAATCTTGAGGAACATCTCCAAGGAACAGGAGGGACTTTGGCTAGAGCCTCTGCTGCTCCCCATCTT
CTCTCTGCCAGAGGCTCTTGGGCTGGCTTGGCTGTGCCCTACCTGTGTCCCGGGCTGACCCCTTCTCTTC
TCTTCTTGTAGACGCTCAGTGTCTTGTCTTGTGCTCCTGGCAAGGCTGAAGAGGCCACTCATCTTC
CTGGGGGGGCTGCCCTCAATGTGGGCTGACCCAGCCAGATCTGAAGGACATTTGGGAGGGGATGCCAGGAA
CGCTCATCTCAGCAGCCTGGGCTGGGATTCGAAGCTGACTTCTATAGGCAATTTGTATCTTGTGAGAA
ATGTGTCACTCCCCCAACCGATTCACTCTTCTCTCTTGTGTAATAATAATAATAATAATAATAATAA

AAAA

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FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDCNDLFLTA
VPPALPAGTQTLLLSQNSIVRVDQSELGYLANLTELDLSQNSFSDARDCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAIILDMNFRPLANLRSLVLGAMNLRREISDYALEGLQSLSELSFYDNQ
LARVPRALEQVPGKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIKFAVNLPL
ELTKLDITNNPRLSFIHPRAFHHLPQMETLMLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPPREMTDHCPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRRLTPAHAGRRYRVYPEGTLELRRTAEAGLYT
CVAQNVLGADTKTVSVVVGRALLQPRDEGQGLELRVQETHPHYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAIILALAVLLLAAGLAAHLGTGQPRKGVGGRRPLPPAWAFWGSAPSVRVV
SAPLVLPWNPGRKLPSSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

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030235-0701

CTACATCGCGAGCGCGCTGTTTCTGAGAGAGGTGAGAAAGTTCCTGGACCCATGTGGAGGAGGGGGACATTTGTGTACCGCCT
 CATCAATCGCGAGACATCATCAAGGTGATCAAGTTTCATCTTCATCATCTGCTACACCGCTCTACTACGTGCACAA
 CATCAAGTTTCGACGTGCACTGCACTGGCATCTTGAGACGCTTACGCGGGTACCGCATCTACCGCTGTGCCAAC
 CCTGGCCACATCTCTTCAAGATCTCTGGCGTCTCTTACATATGACGTATCTGATCTCTACGCGCTTCATCTGTCATGT
 CACACTGTGGTGGATGTCTACGGCGCTCCCTCAAGAAGATCTCGTTTGAGTGATCTCGTGAGGAGACGACGTATGAC
 CGCATCGTCCCGACGTCAAGAACGACATTCGGCTCTCATCTGACCTCATTTGACCAATACAGACCGCGCTTACTCTCAA
 GCGCTCTCGCGCTTCTCTGTCTGGAGTGTAGTGAGAACAGTCTGGCGAGCTGAACCTTCAACACAGGTGTGAGCGT
 GGAACAAGTCTCGGGACGCGCTCACCAAGAACGCGCAGGAACAAGCTGGAAGTGCACCTTGTTCATCTTCAGTGGCT
 CCTGTACACTGTGTGTGACCTGTGTGGAGCTGGAGGTCTTCAAAGTGGAGTCACTCCCGACGTGACCATCCGCGC
 CAGACATGTCGCGACCTACGCGGCTCAAGSAGTGTGGCTTATACCAACAGCGGCGCAAGATTGAAGCGCTGCGCT
 GGCTCTCTCTGGAGAACCTCTCGGGCGCTGCATCAAGTTTACCGACATCAGGAGATCTCCGCTGTGTGATCTA
 TAGCCTTGAGAACATCTGGAGAGTCTGACCTGACGGGCAACTTGAGCGCGGAGAACCAACCGCTCATCTGTCATCGA
 GCGGCTCGGGAGCTCAAAAGCCTCAAGGTGCTCGGGCTTAAGAGAACCTTAAGAGACCTGCCACAGGTGTCTCA
 AGATGTGGGCGTGCACTGACGAAGCTGTCTCATCAACATGAGGGCACAAGCTCATCTGTCTCAACCTTCGACTCAA
 GAAGATGGCGAACATCTGACTGAGCTGGAGCTGATCTCGGCTGCACTGGAGCGACATCCCCCATCTCATCTTCAGCT
 CCACAACTTGACAGAGATGTGACCTCAAGGACCAACCTCAAGAACATCTGAGGAGATCATAGCTTTCAGGACCT
 GACCGGCTTCACTGCCCTTAAGCTGTGTGTGAACCAACACATCTGCCATCTCCCATCAGATGTGGCGAACCTCAACAA
 CTCTGGAGCGGCTTCTACTCAACCGCAACAAGATCGAAGAATCCCAACCACTCTTCTACTTCCGCGAGCTGCG
 CTACTGGACCTTAGCAACAACACTGACCTTCTCTCTCGGACATCTGGCTCTCTGCAAGACTCCAGAGCT
 AGCCATCAGCGGCCAACCGGATCGAGAAGCTCTCTCGGAGACTCTTTCAGTGTCCGGAAGCTCGCGGCTTGCACCT
 GGGCAACAACGTGTCTGACTCACTGCCCTCCAGGTTGGGCGAGCTGACCAACTCAGCATCTGAGCTGCGCGGG
 CACCGGCTTGAAGTGCCTCTGTGTGGAGCTGCGCGAGTCCCACTCGCTCAAGCGCGAGCGGCTGTGTTGTGGAGGG
 GGACCTGTTCAACACATGCCCTCCGAGTGAAGGAGCGGCTCTGGAGGGCTTGACAGAGGACGAGCGCTGAGAGGAG
 GCGCGGCGCACACAGCAGCAGCAGCGCTCGCTCGGACCTCTGAGCGCGGGAGGGCGAGGCTAGTCTTCCCGAG
 AACTCCCGGACAGCCAGGACAGCCTCTCGGCTCGGCGAGGACCTCTGGGCGGCTCTGTGAGTTCAGGCGCAGAGCGAGA
 GGACAGATCTGTGGGCTGAGCCTTCTTCTCTCGAGTACAGTCCCGGAGCAAGTGTCTGTGGAGAGG
 AGCAACTCTCTAGAGCGCGAGTATTTGGATATCAGGTTCTCTCTCGGAGGCGAGCTCTCGCCAGCGGCTGAG
 CTCAACCTAGAGGTTCTTGGGAGCCTCACTTTAGTTCTTGTGATTTATTTTCTTCCATCTCCCACTCTCTTCCTC
 AGATAATCTATACATCTCCCAAGAAATGTCAAGCCAGATGGAGGTGTTCAGGAGAAAGTGGGCTGCTTTTCTCCCT
 TTGTCTTATTTTAGCATGCGCGCGGGCATTTAAACCAACCTGGAATCTCAGCAAGTGTCTCGGCGGCAAGACAG
 CAACTGGAGCGGTCAACCGACGATGCCCGGCTGGGCTCTCGGCTGCGCTCCACGAGGAGGACGAGCGCTCCAGCTGGG
 AAGGCGACAGCTGGAGCTTGCCTCTTCAAGTTTCTTGGCATGTTTASITTTTTGTTTTGTTTTTTTTTATCAAAA
 AAACAAATTTTTTTTTAAAAAAAGCTTTGAAAATCGAGTGTGTGGTATTTAAAAAGAAAAAAATCTAAAAAAA
 AAAAGACATCAACGCGCAGTGGTTGGAATCTGAGGACGAGGTGGCGAGTTTCTCTGAGCAAAAGACGACAGCT
 TGAATCTGTTCTCTTCTTCTCGGCGCAGGCTGAGGCTGTCTCGGATCTGTGTGACCTTGTTCGTCCAGAGTCT
 CTATTGTGTTCTGGGAGGAGGATTTTCTTTGTTGTGTTTGTGGTTTTTTGGTTCTTTTGTCTTTTCTTCTCTCTC
 ATGTGTTCTGCGACGCATCTTCTGTGCTGTGCGGACAGGAAATGTCTTGAGCTTGCAAGGAGGAGGAGGAG
 ACTCGGTTTGGCTAATCCCGGATGAACGTGTCTCAATCTGCACTCTCCCTCTCTGTGCTGCTGCTCTCTCTTCCA
 CGCACAGTGTTAAGGAGCCAGAGGAGCAGCTTCGCCAGACATTTGTTTCCCACTCTCTCGCGGACATGGGTGTGT
 CCAAGTGCACCGCTTGGCTCTCGCTGCTTCATCACTGCTCTGCGCAACCTGTGTCTTCAAGAGACGACATTTA
 GAGCTGTGTGGGATTTGGGAGTGTCCGCTCTGGAGGCGAGGCGCTGTGTCTCAAGCCGGTTCGCGCTTCTGGCGC
 CTGGAGTGTGACACAGCCGACTCGGCACCTGTGGTGTGGAGCGCAACCTGTGTTAGATCATCTGGGTGCCCATCT
 AGAAGGAGTCCCCCGTTAGATCAATCTGCTGACATCAAGGCAAGCTTTAGATGATCTTGTCTCTTAATGATTTATG
 CCACTCGCTCTGCTGCTCAATTGTGTTTCTGCTGCTGTGATGTGATGATCTTCAAGAAATAACTGCACATAG
 CTTCTGACCAACCTAAGAACAAAATTCGTTTACATGTGGGTCTGAACCTGTAGACTCGGCTCACAGTATCAAAATAA
 ATCTTATACAGAAAAAAAAAAA

FIGURE 88

MRQTIISKVIFILIIICYTVVYVHNKFDVDCTVDIESLTGYRTYRCAHPLATLFLKILASFYI
SLVIFYGLICMYTLWWMRLRRSLKKYSFESIREESSYSIDPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRQLNLNNEWTLDKLRQLTKNAQDKLELHFLMLSGIPDVTVFDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLENLRALHIKFTDIKEIPLWI
YSLKTLBELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLQVVVTDVGVLQKLSI
NNEGTKLIVLNSLKKMANLTELIRCDLERIPHSIFSLHNLQEIDLKDNNLKTIEEIIISFQ
HHRLTCLKLWYNHIAIYIPIQIGNLTNLERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFCRKLRLALHLGNNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

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FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCA**ATG**GAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGTGTTGCTGCTGCTGCCGTGCTGCTGGGCGCTGAACGCAGGAGCTGTCAATTGACT
GGCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCGGTTCTAGCACTGGATTGGAAACTTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACTGGCTCCAGGCTGCCAGTCTCCTATTT
GTGGATAATCCCGTGGGCACTGGGTTCA GTTATGTGAATGGTAGTGGTGCCATATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTTCAGTTGCCACAAAG
AATTCAGACAGTTCATTCTACATTTTCTCAGAGTCTTATGGAGGAAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTTATAAGGCCATTCAAGCAGGGACCATCAAGTGAACCTTTCGCGGGGT
TGCTTGGGTGATTCTCGGATCTCCCTGTTGATTCCGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTCTCTTCTCAAGACAAAGGTCTGGCAGAGGTGTCTAAGGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGGTGAACCTTCTATAACATCTTAACATAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTACACAGAGCCACCTAGTTTGTCTTTGTACAGCGC
CACGTGAGACACCTACAACGAGATGCCCTTAAGCCAGCTCATGAATGGCCCCATCAGAAAGAA
GCTCAAATTATTCTGAGGATCAATCCTGGGGAGGCCAGGCTACCAACGTCTTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGAGGCCCTG
GGTGCAGAACTGAAGTGGCCAGAACTGCCTAAATTCACTGAGCTGAAGTGAAGGCCCTGT
ACAGTGACCCTAAATCTTTGAAACATCTGCTTTTGTCAAGTCTACAGAACCCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCATATGGTTCCTTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGACTCAGCAAGAA**TA**GGATGGATGGGGCTGGAGATGAGCTGGTTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGCGCCATTCTTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAGCTTCTGACAGAGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTTCTGCTTCTTAAAAAACCTAAGATTTTTTAAAAAATTGAT
TTGTTTTGATCAAAATAAAGGATGATAATAGATATTAA

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Figure 1

Signal sequence:

N-glycosylation site.

cAMP- and cGMP-dependent protein kinase phosphorylation site.

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGGCGCGCGGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCGGCGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCGCATCGTGGGTGGAGAGGACGCCGAACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCAGGCGGCGCACTGCTTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTTGGCCAGCTGACTTCCATGCCATCCTTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCCTGCACCTGTCACTTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTTGAGTTTGAGAACCGACAGACTGCTGGGTGACTGGCTGGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCTCCAGGAAGTTCAGGTCGCCATCATAAACA
ACTCTATGTGAACACCTCTTCCTCAAGTACAGTTTCCGCAAGGACATCTTTGGAGACATG
GTTTGTGCTGGCAACGCCCAAGGCGGGAAGGATGCCTGCTTCGGTGACTCAGGTGGACCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGGAGTGGGCTGTG
GTCGGCCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTGTAGTGGATCCAGAAG
CTGATGGCCCAAGAGTGGCATGTCCAGCCAGACCCCTCCTGGCCACTACTCTTTTCCCTCT
TCTCTGGGCTCTCCCACTCCTGGGGCGGTCTTGAGCCTACCTGAGCCCATGCAGCCTGGGGC
CACTGCCAAGTCAGGCCCTGGTCTCTTCTGTCTTGTGTTGGTAAATAAACACATTCCAGTTGA
TGCTTGCAGGGCATCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 92

MGARGALLLALLLARAGLRKPESQEAPLSGFCGRVITSRIVGGEDAELGRWPWQGSRLRW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSFYDIALVKLSAFVTTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVQVAIIINNSMCNHLFLKYSFRKDI FGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNRPGVYTNISHHFEWIKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

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FIGURE 93

CCCA CGCGTCCGCGGACGCGTGGGAAGGGCAGAAATGGGACTCCAAGCCTGCCTCCTAGGGCT
CTTTGCCCTCATCTCTCTGGCAAATGCAGTTACAGCCCGGAGCCCCGACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGTCCTTGGGCCGTGCGGACCTTGAGGAAGAGCTGAGTCTCACCTTT
GCCTTGAGACAGCAGAATGTGGAAAGACTCTCGGAGCTGGTGCAAGGCTGTGTGCGATCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCCTCCACACGGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTTCTGACTTGCTGGCTGAGCATCCGACAAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTTTCATCACTATGTGGGAGGACCTACGGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTTGGCCCCCATGTGGACTTTGTGGGGGGACTGCAACCGT
TTTCCCCCAACATCATCCCTGAGGCAACGTCTTGAGCCGCAAGGTGACAGGGAAGTGTAGGCCT
GCATCTGGGGGTAAACCCCTCTGTGATCCGTAAAGCGATACAACCTTGACCTCACAGACGTGG
GCTCTGGCACCCAGCAATAACAGCCAGCCTGTGCCAGTTCCCTGGAGCAGTATTTCCATGAC
TCAGACTTGCTCAGTTTCATGCGCTCTTTCGGTGGCAACTTTGCACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGCCGGGATTTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGCTGGTGCCAAACATCTCCACCTGGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCTGTCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGGCCATGAT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA
AGCTGAGCTCATGAAGGTGCCGCTCGGGGTCTCACCTGCTCTTCGCCTCAGGTGACAGT
GCGGCCGGGTGAGTCTGTCTCTGGAAGACACCAAGTTCCGCCCTACTTCCCTGCCCTCCAG
CCCCATATGTCACCAAGTGGGAGGCACATCCTTCCAGGAACCTTTCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGTGGCTTTCAGCAATGTGTTCCCAACGGCTTCATACAGGAG
GAAGCTGTAAACGAAGTTTCTGAGCTTAGCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCCGTGCCATACCAGATGTGGCTGCACTTTCTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCCATTCATGGGTGTCGGAACTCGGCCCTCTACTCCAGTGTTTGGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTTAGTGGCCGCCCCCTCTGGCTTCTCAACCCAAAG
GCTCTACCAGCAGCATGGGGCAGGTCTCTTTGATGTAAACCGTGGCTGCCATGAGTCTCTGT
TGGATGAAGAGGTAGAGGGCCAGGGTTTCTGCTCTGGTCTTGCTGGATCCTGTAAACAGGC
TGGGGAACACCAACTTCCAGCTTTGCTGAAGACTCTACTCAACCCCTGACCCCTTTCCTATC
AGGAGAGATGGCTTGTCCTCCCTGCCCTGAAGCTGGCAGTTTCAGTCCCTTATTCTGCCCTGTTG
GAAGCCCTGTGAACCTTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCGAAA
TGCTGTGAGCTTGACTTGACTCCCAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTTAGATTCTCAATAAGATGCTGTAAGTACGATTTTTTGAATGCCCTCTCCCTCCGC
ATCTCATCTTTCTCTTTCAATCAGGCTTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCATCTGATATTCAATCCCCAATTCAGTGAAGGAGACCTCTACTGTCAACCGTTTACTCT
TTCCCTACCCTGATCATCAGAAACAAATGGCCTCAGTGCACTACTCTCAATCTTTGCTTTATG
GCCCTTTCATCATAGTTGCCCCACTCCCTCTCCTTACTAGCTTCCAGGTCTTAACTTCTCTG
ACTACTCTTGCTTCTCTCTCATCAATTCTGCTCTCTCATGGAATGCTGACCTTCAATGC
TCCATTGTAGATTTTTGCTCTTCTCAGTTTACTCATTGTCCCTTGGAAACAAATCACTGACA
TGTACAACCATTACCATCTCACTAAATAAGACTTTCTATCCAATAATGATTGATACCTCAAA
TGTAAAAAA

05902615.071001

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLP PGWVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGYKLTLENVADLVRPSPLTLHTVQKWL LAAGA QKCHSVITQDFLTCWL
SIRQAELLPGA EFHHYVGGPTETHVVRSPHPYQLPQALAPHVDFVGG LHRFPPTSSLRQRP
EPQVTGTVGLHLGVTSPVIRKRYNLTSQDVGSGTSNNSQACAQFLEQYFHDSDLAQFMRLF
GNFAHQASVARVVGQQGRAGIEASLDVQYLMSAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDD EDSLSSAYIQRVNTELMKAAARGLTLLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTITVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPFSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVPFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWD PVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

03902615.071001

FIGURE 95

GCCGCGCGCTCTCTCCCGCGCCACACCTGTCTGAGCGGCGCAGCGAGCCGCGGCCCGGGC
GGGCTGCTCGGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTCTC
TTCTTTCTGCTCTGTGCTGTTGGGCAAGTGAGCCCTTACAGTGCCCCCTGGAAACCACTTG
GCCTGCATACCGCCTCCTGTGCTCTTGCCCCAGTCTACCTCAATTTAGCCAAGCCAGACT
TTGGAGCCGAAGCCAAATTAGAAGTATCTTCTTCAATGTGGACCCCACTGTCTATAAGGGA
CCACTGCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTTATGGCTATGACAGC
AGGTTTCAGCATTTTTGGGAAGGACTTCCTGCTCAACTACCTTTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGGCACCTGCTGGCAGAGAAGCATGTCCTCACAGCTGCCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAAGCTTCGAGTGGGCTTCCTAAAGCCC
AAGTTTAAAGATGCTGCTGAGGGGCCAAGCACTCCACTTCAGCATGCCCGAGCAGATGAA
ATTTTCAGTGGATCCGGGTGAAACGCACCCATGTGCCCAAGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCCTGCTAAGCAGCTGCCAGGGGGCAGAATTCACCTTCTC
TGGTATGACAATGACCGACAGGCAATTTGGTGTATCGCTTCTGTGACGTCAAAGACGAGA
CCTATGACTTGTCTCTACCAGCAATGCGATGCCCAGCCAGGGGCCAGCGGGTCTGGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAAGTGGGAGCGAAAAATTATTGGCATTTTTTTCAGG
GCACCACTGGGTGGACATGAATGGTTCCCCACAGGATTTCAACGTGGCTGTGAGAATCACTC
CTCTCAAAATATGCCCAGATTTGCTATTTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTTCCCTCCTGGCAGCAATTAAGGGTCTTTCATGTTCTTATTTTAGGAGAGGCC
AAATTGTTTTTTGTTCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTGTGTGAAGGTGT
CTTATAATCTTTTACCTATTTCTTACAATTGCAAGATGACTGGCTTTACTATTTGAAAATG
GTTTGTGTATCATATCATATATCATTAAAGCAGTTTGAAGGCATACTTTTGCATAGAAATAA
AAAAAACTAGATTTGGGGCAATGAGGAATATTTGACAATTAAGTTAATCTTCACGTTTTTG
CAAACCTTGATTTTTTATTTTCATCTGAACCTGTTTCAAAGATTTATATTAATATTTGGCATA
CAAGAGATATGAAAAAAAAAAAAAAAAA

0902815.071001

FIGURE 96

MAGIPGLLFLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLAKPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVGIIYLSSSGDGAQHRDSGSSGKS
RRKRQIYGYSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTAAHCIHDGKTYVKG
TQKL RVGFLKPKFKDGGRGANDSTSAMPEQMKFQWIRVKRTHVPKGWIKGNANDIGMDYDYA
LLELKKPHKRKFMKIGVSPPAKQLPGGRIHFSGYDNDRPGNLVYR FCDVKDETYDLLYQQCD
AQPGASGSGVYVRMWKRQQQKWERKIIGIFSGHQWVDMNGSPQDFNVAVRITPLKYAQCICYW
IKGNYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

090815.071001

FIGURE 97

GCATCGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCCCACCAGGCCATGGTGGTTT
CTGGAGCGCCCCAGCCTGGGTGGGGGCTGTCTCGGCACCTTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACCTGTTCCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGGTTGTGGGCGGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTCTGCTCACCAGCCGCTGGGTGATC
ACTGCTGCCCCACTGTTTCAAGGACAACTGAACAAACCATACTGTCTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGGAAACCTGGCTCTCGGTCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCCCCTGTGTATTCTCGAAGGAAGGTGCCTGTGCAGACATTGCCTGGTGCCTCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGTCTGCCCATCTGCCTACCTGATGCCTCTATCCACCT
CCCTCCAAACACCCA CTGCTGGATCTCAGGCTGGGGGAGCATCCAAGATGGAGTTCCTTGC
CCCACCTCAGACCCTGCAGAAGCTGAAGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGGAGCAGGACAGGACCCATCACTGAGGACATGCTGTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGCTGGGCGACTCCGGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCGAGCGCAACAGGCCC
GGGGTCTACATCAGCCTCTCTGCGCACCGCTCCTGGGTGGAGAAGATCGTGCAAGGGGTGCA
GCTCCGCGGGCGCGCTCAGGGGGGTGGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGGCCG
CCGCGCGCTCCTAGGGCGCAGCGGGACGCGGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGGCGGTTTCCCCCGCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCCGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCCCAACGGCCTCATGTCCCCGCCCCCAC
GACTTCCGGCCCCCGCCCCGGGCCCCAGCGCTTTGTGTATATAAATGTTAATGATTTTTAT
AGGTATTTGTAACCTGCCACATATCTTATTTATTCCTCCAATTTCAATAAATATTTATT
CTCAAAAAAAAAA

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05025-07103

Signal sequence:

N-glycosylation site.

Glycosaminoglycan attachment site.

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACC**ATG**CACGGCTCCTGCAGTTTCTGTAGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCGTTGGAGCCCTCACAGATGAGGAGAAACGTTTGATGGT
GGAGCTGCACAACTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTTCGCCAAGGCCTACGCACGGCAGTGCGTGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGCGGAGAAATCTGTTCCGCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGACCACGAGCGTGAGCACTACAACCTCAGCGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGGCCAAGACAGAGAGGATC
GGCTGTGGTTCCCACTTCTGTGAGAAGCTCCAGGGTGTTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGGAACGTGAAGGGGAAACGGCCCTACCAGGAGGGGAACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGAAGATGCTCAGGATTTGCCTTACCTGGTAACTGAGGCCCATCCTTCCGGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTTCTTCCCTAGCAACGGGGATTCCGGCTTTCT
TGTTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACTTCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCCACCTTGCGTAACT
AACTGAGGTCCCTTCCATTTTGGCAGCTCACAGCCTGCCCTCCTTGATGAGGAGCCAGTTA
CCTTCCCAAATCGACCCATGTTCTCTATCCCAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGGCAAG
GGAACCTCTACCCATGCCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCTTCCAGTG
AGGTCTTGCCCTCAGTTTTCAGCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGACACCTCTCCAAAGTCCCTGCCCAATTTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGGCGTGCCCTGGCTCTGCAGTCGTCTTGCCAGGTGCAGAGGGCCCTGACA
AGCCTAGCGTGTGTGTCAGGGCTGAACTCGGGCCCTGGTCATGTGTGGGGCCCTCTCTGGGA
CTACTGCTCCTGCCTCCTCTGGTGTGGCTGGAATCTT**TGA**ATGGGATACCACTCAAAGGG
TGAAGAGGTGAGCTGTCTCTGTGATCTTCCCCACCTGTCCCCAGCCCTAAACAAGATA
CTTCTTGGTTAAGGCCCTCCGGGAAGGGAAAGGCTACGGGGCATGTGCCTCATCACACCATCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCGCTGAGGACTGCACACC
GGGCCACACCTCTCTGCCCCCTCCTCCTGAGTCTGGGGTGAGGAGATTGAGGGAGCT
CACTGCTTACCTGGCTGGGGCTGTCTGCCACACAGCATGTGCGCTCTCCCTGAGTGCCTG
TGTAAGTGGGATGGGGATTCTTAGGGGAGATGAAGGACAAGCCCCACTGGAGTGGGGTTC
TTTGTGAGTGGGGAGGCAGGGACGAGGGAAGGAAAGTAACCTCCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

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FIGURE 100

MHGSCSFLMLLLPLLLLLLVATTGFPVGALTDEEKRLMVELHNLRYAQVSPTASDMLHMRWDEE
LAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVETNIELLVCNYPGPNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEDAQDLPLYLVTEAPSPFRATEASDSRKMGTTPSSLATGIPAFVLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPVCVTEVPSILAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKTKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLAS
VFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSV
SGLNSGPGHVGPLLGLLLPPLVLGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACTGAAGTCAGGCTTTTCATTGGGAAGCCCCCTCAACAGAAATTCGGTCATTCTCCAAGTATATGGTGAGCAGT
ACTCTGTGTGTTCTCCCTCTGCTTGCTTTTTCAATTAGCAGACCGGACTTAAGTCACAAAGATTAATCTTTTCAAT
CAAGGCAAGTTCATGAGCCACCTTCAAAGCCTTCGAGAAGTGAAACTGAAACAACAAATGAATGGAGACCATTC
AAATCTGGGACCAAGTCTCGGCAAAATATACACTTCTCTCCTTGGCTGGAAACAGGATTTGTGAATACTCCCTGA
ACATCTGAAAGAGTTTTCAGTCCCTTGAAACTTTGGACCTTAGCAGCAACAAATTTTCAGAGCTCCAAAGCTCAT
TCCGACCTCAGCTCAAATATCTGTATCTCAAAGCAACCGAGTCACATCAATGGAACTCGGATTTTGAACAA
TTTGGCCAAACACACTCTTGTGTTTAAAGCTGAAACAGGAACCGAATCTCAGCTATCCCAACCAAGATGTTTAAACT
GCCCACTGCAACATCTGCAATTTGAAACCGAAACAGAGTAAAAATGTAGATGGAGTCAGATTCCAAGGCTTGG
TGCTCTGAAGTCTCTGAAAGTGCAGAAAGATGGAGTAACGAAACTTTATGGATGGAGCTTTTGGGGGCTGAGCAA
CATGGAAATTTCTCAGCTGGACCATAAACAACTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTCTGTATGCT
GCAGAGACTTTCATCTCAGCCAAAATGCCATCAACAGAGTCAGCCCTGATGGCTGGAGGTTCTGCCAGAAAGCTCAG
TGAGCTGGAGCTTAATTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTCTGGCCCTTAAGCTTACTAAATAC
ACTGCACATTTGGGAACAACAGAGTCAGCTACATTGCTGATTGTGCTTCCGGGGCTTTCCAGTTTAAAGACTTT
GGATCTGAAGAACAAATGAATTTCTGGACTATTGAAGACATGAATGGTGCTTTCTCTGGGCTTGAACAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAGGCTTCTTCACTGGTTGGATGCTATGGAGCA
CTAGACCTGAGTGACAAAGCAATCATGCTTTTACAAAGGCAATGCATTTTCAAAATGAAGAAATCGCAACAAAT
GCATTTAAATACATCAAGCTTTTGTGGGATTCGCACTTAAATGGCTCCCACTGAGTGGGTGGCGGAAACCACTT
TCAGAGCTTTGTAATGCCAGTTGTGCCCATCTCAGCTGCTAAAGGAAGAAGCATTTTGTCTGTAGCCAGA
TGGCTTTGTGTGTGATGATTTTCCCAACCCAGATCAGGTTTCAGCCAGAACACAGTCCGCAATAAAGGTTTC
CAATTTGAGTTTCTCATCTCAGCTGCCAGCAGCAGTGATTCCCAATGACTTTTGTCTGGAAATGAACAATG
ACTACTGCATGCTGTAATTTGGAATTTATGACACCTCCCGGGCCCAAGGTGGCGAGGTGATGGAGTATACAC
CATCTCTCGGCTGCGGAGGTGGAATTTGCGAGTGAGGGGAAATATCAGTGTGCTTCCATCACTTTGGTTT
ATCTCACTCTGTCTCAAAGCCAGCTTACAGTAAATATGCTTCCCTCATTACCAAGACCCCCATGGATCTCACAT
CCGAGCTGGGGCCATGGCAGCTTGGAGTGTGCTGTGTGGGGCACCCAGCCCCAGATAGCCTGGCAGAGGA
TGGGGGCACAGACTTCCAGCTGCACGGGAGAGACGATGCATGTGATGCCGAGGATGACGTGTTTCTTTATGCT
GGATGTGAAGATAGAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGTATTTGGCAAAATGC
AACTCTGACTGTCTAGAAACACCATCATTTTGGCGCCACTGTGGACCGAACTGTAAACAAAGGAGAAACAGC
CGTCTACAGTGCATCTGGAGGAAGCCCTCCCCCTAACTGAACCTGGACCAAGATGATAGCCCATTTGGTGTG
AACCAGAGGACATTTTTGACAGAGGCAATCAGCTTCTGATTATTGTGGATCAGATGTCAAGTATGCTGGGAA
ATACACATGTGAGATGCTAAACCCCTTGGCACTGAGAGAGGAAACGTCGCTCAGTGTGATCCCCACTCCAA
CTGGCACTCCCCCAGATGACAGCCCCATCGTTAGACGATGACGGATGGGCCACTGTGGGTGTGCTGATCATAGC
CGTGGTTTGTCTGTGTGGTGGGCACTCACTCGTGTGGGTGCTCATCATATACCAACAAGGCGGAGGAATGAAGA
TTGCAGCATTACCAACAGATGAGACCAACTTCCAGCAGATATTCTTGAATTTTGTCTATCTCAGGGAACGTT
AGCTGACAGCGAGGATGGGTACGTGTCTTCAAGAAAGTGAAGCCACCCAGTTTGTCACTCTCAGGTGCTGG
ATTTTCTTACCAACAATGACAGTAGTGGGACCTGCCATATTGACAAATAGCAGTGAAGCTGATGTGGAAAGCTGC
CACAGATCTGTTCTTGTTCGTTTGGGATCCAAGGCCCTATGTATTGAAGGGAATGTGTATGGCTCAGA
TCTTTTGAACATATCATACAGTTGCACTGCTACCCAGAAACAGTTTTAAATGGACCCATAGAGCCAGTTA
CATAAAGAAAGAGGAGTGCATACCATGTTCTCATCTTCAAGAAGATCCTGCGAACCGAGCTCAGTAATATTC
GTGGCCTTCACTGTGAGGAAGCTACTTAACTAGTTACTCTCACAATGAAGGACCTGGAATGAAAAATCTGTG
TCTAAACAGACTCCTCTTTGATTTTAAAGTGCAAATCCAGAGCCAGCGTCGGTTCTCGCTCGAGTAACTTTTATGGG
TACCTTTGGAAAGCTCTCAGGAGACCTCACCTAGATGCTTATTCAGCTTTGGACAGCCATCAGATTGTCAAGC
AAGAGCTTTTATTTGAAAGCTCATTTCTCCAGACTTGGACTCGGGTCAGAGAGATGGGAAAGAAAGGAC
AGATTTTCAGGAAGAAATACATTTGTACCTTTAAACAGACTTAGAAACTACAGGACTCCAAATTTTTCAGTC
TATGACTTGGACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACCTCAAGTGAACCTTTTATTTA
AAAGAGAGAGAACTTATGTTTTTTAAATGGAGTTATGAATTTTAAAGGATTAATAATGCTTTATTTATACAGAT
GAACCAAAATTAACAAAGTTTATGAATTTTATATCGGGAATGATGCTCATATTAAGATACCTTTTAAACTA
TTTTTTAACTTTGTTTATGCAAAAGATATCTTACGTAAATTAATGATTAATATGATTTTATGTATTT
TTATATGCGCAAGTTCTTTTATGGAAGATGAGTTACTAAAGCATTTTAAATATACCTGCTCTGTACATTTT
TTAAATAGAAGTTACTTCATTATATTTTGCACATTTATTTTAAATAAATGTGTCAATTTGAA

FIGURE 102

MVDVLLFLSLCLLFHISRDLSHNRSLFIKASSMSHLQSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFAPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNIRISAI PPKMFKL PQLQHLBELNRNKIKNV DGLTFQGLGALKSLKM
QRNGVTKLMDGAFWGLSNMBEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWE
FCQKLSLELDLTFNHLSRLDDSSFLGLSLNLTLHIGNNRVSYIADCAFRGLSSSLKTLDLKNE
ISWITIEDMNGAFSGLDKLRLLIQGNRIRISITKKAFTGLDALEHLDSLDAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPPQWVAENNFQSFVNASCAPHQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNL SFICSAASSSDSPMTFAWKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTTPMDLTIRAGA
MARLECAAVGHAPQIAWQKDG GTDPPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTTKGETAVLQCIAGGSPPPKLNWTKDDSPLVVTER
HFFAAGNQLLIIVSDSDVSGAKYTCESNTLGTTERGNVRLSVIPTPTCDSPQMTAPSLDDDG
WATVGVVIIAVVCCVVGTSVLVWVVIYHTRRRNEDCSI TNDTETNL PADIPSYLSSQGTLD
RQDGYVSSSESGSHHQVFTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYSGDPFETYHTGCSGDPRTVLMDHYEPSYIKKKECYPCSHPSSESCERSFSNLSW
PSHVRKLLNTSYSHNEGPGMKNLCLNKSSLD FSANPEPASVASSNSFMGTGPKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQS
YLDLT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAATG
AAGGATGCAAGGACGAGCTTTCTCTGGAAACGGAACGCAATGGATAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTTTCTTGTGAGCCCTGGATCTTAAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGATGAAA
TAAACAGAGATTAGACCCCGGGGGTGGTGTGTTCTGACATAAATAAATAATCTTAAAGCAGCTGTTCCCTCTCC
CCACCCCCAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGTATGTTTCATTTTTCTC
TATAAAGGAGAAACTGAGCCCAAGGAGATATTTTTGGAATGAAAAGTTTGGGGCTTTTATTAGTAAAGTAAAGAACT
GGTGGTGGTGTTTTTGCTTTCTTTTGAATTTCCCAACAGAGGAGAGGAAATTAATAATACATCTGCAAGAAA
TTTCAGAGAGAAAAGTTGACCGCGGCAGATTGAGGCATTGATTGGGGGAGAGAAAACGACAGAGACACATTGGGA
TTTGTGCCATTGTTGACTAAAATTGACGGATAATTGCAATTGGATTTTCTTCATCAACTCCCTTTTTTTTAAAT
TTTTATTCTCTTTGGTATCAAGATCATGCGTTTTCTCTGTCTTAAACCACTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAATACAACTGTTTGAATTCAGAGAGGACCAACACAGATAAATTAATGATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCTAGGTTTAAACAGGCCCTATTTGACCCCTGCTTGTGGTGTCT
GCTGGCTCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGCGGCTCAGACCTGCGCTTCTGTGTGCTCCTGCAGCAA
CCAGTTTCAGCAAGGTGATTGTGTTCGGAACCACTGCGGAGGTTCGGATGGCATCTCCACCAACACACGGCT
GCTGAACCTCCATGAGAACCAATCCAGATCAACAAAGTGAACAGCTTCAAGCACTTGAGGCATTGGAAATCCT
ACAGTTGATAGGAACCATATCAGAACCATGAAATTTGGGGCTTTCAATGCTTGGCGAACCTCAACACTCTGGA
ACTCTTTGACAATCCTCTTACTACACTCCGAATGGAGCTTTGTATACTTGTCTAAACTGAAGGAGCTTGGTT
GCGAAACCAACCCATGAAAGCATCCCTCTTATGCTTTTAAACGAATTCCTCTTTGGCGGCACTAGACTAGG
GGAATTGCAAAAGCTTTCATACATCTCAGAAGGTGCCCTTGAAGGTCTGTCCAATGTAGGTATTGAACTTGG
CATGTGCAACCTTCGGGAAATCCCTAACCTTCACACGCTCTATAAACTAGATGAGCTGATATTCTTGGGAATCA
TTTATCTGCGCATCAGCCCTGGCTCTTTCCAGGGTTTGTGACACTTCAAAACTGTGGATGATACAGCCAGAT
TCAAGTTAGTGAACGGAATGCCCTTTGACAACCTTCAGTCACCTAGTGGAGCTCAACTGGCACAATAATCTTAAC
ATTACTGCTCATGACCTCTTCACTCCCTTGCAATCATCTAGAGCGGATACATTAATACATCAACACCTTGGAACTG
TAACCTGTGACATATGTGGCTGAGCTGGTGGATAAAGACATGGCCCTCGAACAGCACTGTTGTGGCCGGTG
TAACACTCTCTCCCAATCAAGAGGGAGGTACATTGGAGAGCTCGACAGAAATTAATTCATCATGCTCTAGTCTCGGT
GATTGTGGAGGCCCTTCAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAAATGTGGGGCTCCACATC
CCTGACATCTGATCTTGGATTACTCCTCAATGTGAACAGTCAATGACACATGGGGCGTACAAAGTGGCGATAGCTGT
GCTCAGTGATGGTACGTTAAATTTCACAAAATGTAACCTGTGCAAGATACAGGCCATGTACATGATGTTGGTGAAT
TTCCGTTGGGAATACTACTGCTTCAGCAACCTTGAATGTTACTGACAGCAACCACTACTCTCTTCTCTTACTTTTC
AACCCTCAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACGGACCAAGATACAAATGTGGGTCCCACTCC
AGTGGTCGACTGGAGACCAACCAATGTGACCACTCTCTCACACCAACAGACCAAGGTGACAGAGAAAACCTT
CACCATCCCACTGACTGATATAAACAGTGGGATCCCAAGAAATGTGAGGTATGAAAGCTACCAAAATCATCAT
TGGGTGTTTTTGTGGCCATCACTCATGCTGCACTGATGCTGCTCATTTCTACAAGATGAGGAAGCAGACCA
TCGGCAAACCACTCAGCCCCAACAGGACTGTTGAAATTTATTAATGTGGATGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCCATGCCCTGCTATCGAGCATGAGCACTAAATCACTATAACTCATACAAATCTCCCTT
CAACACACACAACAGTTTAAACAATAAATTCAAATACAGTTTACAGATTACAGATGAAACCGTTATTGATCCGAATGAA
CTCTAAAGCAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACCAACAAATCAAAAAA
GACAGTTTATTAATAAATGACACAAATGACTGGCTAAATCTACTGTTTCAAAAAAGGTGCTTTACAAAAA
AAAAAGAAAGAAATTTATTTATTAATAAATCTTATGTGATCTAAAGCAGACAAAA

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FIGURE 104

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLNLHENQIQIIVKNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAPEGLSNLRYLNLAMCNLREIPNLTLPLIKLDELDSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLEIRIHLHHNPWNCNDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVDQTMGYTCMVNSVGN
TTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKFTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHRQN
HHAPTRTVEIINVDDEITGDTPMESHLPMPAIEHEHLNHYSYKSPFNHNTTNTVNTINSIHS
VHEPLLRIMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

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FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGCAGTTGCGAGTTCTTTTCGGTTTCCCTCCTGCTGTTTGGGGGCA
TGAAAGGGCTTCGCCGCGCCGAGTAAAGAAGAAATGACCGGGCAGCGCGAGGGAGGAGCGCCACGCCGACCGC
GAGGGCGGGCGCTGCACCTTCGGCTGGAAGTTTTCGCCGGCCCGAGCGCGCGCTGGGAGCTTCGGGTAGA
GACCTTAGCGCTGGAACCGGCTGAGCGCGCGAGCCTCCGTCGCGCGCGCGGGGTTGGGGCTGCTGCTGTGC
GCGGTGCTGGGGCGCGCTGGCGGTCCGACACGCGGGTCCGGGGAACTCGGGCAGCCCTCTGGGGTAGCGCG
GAGCGCCCATGCCCACTACCTGCCCTGCCCTCGGGGACCTGCTGGACTGCAGTCGTAAGCGGTAGCGCGCTCT
CCGAGCCACTCCGCTCTGGGTGCTGCTGGCTGGACTTAAGTCAACAAGATTATCTTTCACTCAAGGCAAGTTCC
ATGAGCCACTTCAAAGCCTTCGAGAAGTGAACATGAACACAAATGAATGGAGACCATCCAAATCTGGGACCA
GTCTCGGCAAAATTTACCTTCTCTCCTGGCTGGAAACAGGATTTGTGAATACTCCCGAACTCTGAAAGAG
TTTCAGTCCCTTGAACCTTTGGACCTTAGCAGCACAAATATTTTCAGAGCTCCAACTGCATTTCCAGCCCTACAG
CTCAAAATATCTGTATCTCAACAGCAACCGAGTCACTCAATGGAACTCGGGTATTTTGACAATTTGGGCCAACACA
CTCCTTGTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCACCCAAAGATGTTTAACTGCCCCAACTGCA
CATCTCGAATTAACACGAAACAGATTAAAAATGTAGATGGACTGACATTCGAAGCCCTGGTGCTCTGGAATCT
CTGAAAATGCAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTTGGGGGCTGAGCAACATGGAATTTTG
CAGCTGGACCAATAACAACCTAACAGAGATTACCAAGGCTGGCTTTACGGCTTGTGTGATGCTGCAGGAACCTCAT
CTCAGCCAAAATGCCATCAAGCAGGATCAGCCCTGATGCCCTGGGAGTTCTGCCAGAGCTCAGTGAGCTGGACCTA
ACTTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTTCTTGGCTTAAGCTTCTGCGGCTGACAACTGAGGAGCTGAG
AACACACAGAGTCAGCTACATTTGTGATTTGTGCTTCCGGGGCTTCCAGTTTAAAGACTTTGGATCTGAAGAAC
AATGAAATTTCTGAGCTATTGAAGCACTGAATGGTGTCTTCTGCGGCTGACAACTGAGGCGAGCTACATCTC
CAAGGAAATCGGATCGGTTCTTATTAATAAAAAAGCCTTCACTGTTTGGATGATTTGAGCATCTAGACCTGAGT
GACACCGCAATCATGTCTTTTCAAGGCAATGCAATTTTCAAAATGAAGAACTGCAAAATGCATTTTAAATACA
TCAAGCCTTTTGTGGCATTTGGCAGCTAAATGGCTCCACAGTGGGTGGCGGCAAAACAACTTTCAAGCTTTGTA
ATAGCCAGTTGTGCGCACTCTCAGCTGTAAAGGAAGAAGCATTTTGTGTTAGCCAGATGSCCTTTGTGTGT
GATGATTTTCCCAAAACCCAGATCAAGGTTTACGCGAGAACACAGTGGGCAATAAAGGTTTCAATTTGAGTTTC
ATCTGCTCAGCTGCGACGAGCAGTGAATTCGCAATGACTTTTGTGTAAGAAAGAACATGAATCTACGATGAT
GCTGAAATGGAATTTATGCAACCTCCGGGCCCAAGGTGGCGAGTATGAGATATACCACATCTCTCGGCTG
CTCAGGCTGGAATTTGCGAGTAGGGGAAATATCAGTGTCTCATCTCCATGATCTTGGTTTCATCTACTCTGTCT
AAAGCCAGGCTTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCATGGATCTCCATCTCGAGCTGGGGCC
ATGGCACGCTTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCTGGCAGAGGATGGGGCACAGAC
TTCCAGCTGCGAGGGGAGAGCGCATGCTGATGCCCGAGGATGACGCTGTTCTTTATCGTGGATGTGAAGATA
GAGGACATTTGGGTATACAGCTGCACAGCTCAGAACAGTGCAGGAAGATTTCAGCAAAATGCAACTCTGACTGTCT
CTAGAAAACACCATCATTTTTCGGGCACTGTTTGGACGAACTGTAAACCAAGGGAGAAACAGCCGCTCACAGTGC
AATGCTGAGGAGGAGCCCTCCCCCTAAACTGAACTGGACCAAAAGATGATAGCCCATTTGTTGGTAAACGAGAGGAC
TTTTTTCAGCAGGCAATCAGCTCTCTGATTTATTTGGAGCTCAGATGCTCAGTGATGCTGGGAAATACATATGTGAG
ATGCTTAACACCCCTTGGCACTGAGAGAGGAAACGCTGGCGCTCAGTGTGATCCCCACTCCAACTCGGACTCTCCCT
CAGATGACAGCCGATCGTTAGACGATGACGGATGGGCACTGTGGGTGCTGTGATCATAGCCGCTGGTTCTGCTGT
GTGTTGGGCAGTCACTCGTGTGGGTGCTCATATAACACACAAGCGCGAGGAATGAAGTTTCAGGACATTACC
AACACAGATGAGCCCACTTGCAGCAGATATCTCTAGTTATTTGTGATCTCAGGAACTGAGGAACTGAGCTGTGCT
GATGGGTACGTGCTTTCAGAAAGTGAAGGCCACCAACAGTTTGTCAATCTTCAGTGCTGGATTTTCTTACCA
CAACATGACAGTAGTGGGACCTGCCATATTTGACAAATAGCAGTGAAGCTGTGGAAGCTGCCACAGATCTGTCT
CTTTGTGCTGTTTGGGATCCACAGGCCCTATGATTTTGAAGGAAATGTGTATGGCTCAGATCTTTTGAACA
TATCATACAGTTGAGCTCCTGACCCCAAGAACATTTTGAATGGACCACTATGAGGCCAGTTACATAAAGAAAAG
GAGTGCACCACTGTTCTCATCTCTTCAAGAAATCCTGCGAAGCGGAGCTTCAGTAATATATCTGTGGCCTTCACAT
GTGAGGAAGCTCTTAACTAGTCTTCTCAGATGAGGAGCTTGAATGAAGAAATCTGTGTTCAAAACAGTCTC
TCTTTAGATTTTAGTGCAAACTCAGAGCCAGCGTGGTTCCTCAGTAATCTTTTCATGGGTACCTTTTGAAGAA
GCTCTCAGGAGACTTCCATAGAGTGCCCTTCAAGCTTTGGACAGCCATCAGATGTGACGCAAGAGCCCTTTAT
TTGAAGCTCATCTTCTCCAGACTTGGACTCTGGGTGAGGAGAGATGGGAAAGAAAGGACAGATTTTCAGGAA
GAAATCATTTTGTACTCTTTTAAACAGACTTTAGAAAATCTCAGGACTCCAAATTTTTCAGTCTTATGACTGTGAC
ACATAGACTGAATGAGACCAAGGAAAGCTTAACTACTACTCTCAAGTGAATCTTTTATTTAAAGAGAGAGAT
CTTATGTTTTTTAAATGAGATTGAATTTTAAAGGATAAAATGCTTTTATGATTTTATGATTTTATGATGAGGACA
AAAAGTTATGAAAATTTTATGACTGGGAATGATGCTCATATAAGAACTCTTTTAACTATTTTAACTTTG
TTTATGCAAAAAGTATCTTACGTGATAATTAATCATGATTTTATGATTTTATGATTTTATGATGAGGACA
TTTCTTTTATGAAAATGAGTTACTTAAAGCAATTTTAAATATACCTGCTGTTACCATTTTAAATAGAGTT
ACTTCATATATTTTGCACATTTATTTTAAATAATGTGTCATTTTGAAGAAAAA

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FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCIGDLLDCSR
KRLARLPEPLPSWVARLDLSDHNLRSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDDLSSNNISELQTAFFPALQLKLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNISAI PPKMFKLPQLQHLELNRRNKIKNV DGLTFQGLGALKSLKMQR
NGVTKLMDGAFWGLSNMEILQLDHNHNLTEITKGWLYGLLMLQELHLSQNAINRISPDWAEFC
QKLSLELDLTFNHL SRLDDSSFLGLSLNLT LHIGNNRVSYIADCAFRGLSSSLKTLDLKNNIEIS
WTIEDMNGAFSGLDKLRLILQGNRIRISITTKAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQQLHLNLTSSLLDCQLKWL PQWVAENNFQSFVNASC AHPQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKNELLHDAEMENYAH LRAQGGE
VMEYTTILRLREVEFASSEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTI RAGAMA
RLECAAVGHGPAQIAWQKDGGTDFPAARERRMHVMPEDDVFFI VDKIEDIGVYSTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTVKGETAVLQCIAGGSPPPKLNWTKDSDPLV VTERHF
FAAGNQLLIIVDS DVS DAKYTC EMSNTLTGTERGNVRLSVIPTPTCDSPQMTAPSLDDDGWA
TVGVVIIAVVCCVVGTSLVWVVIIYHTRRRNEDCSITNTDETNL PADIPSYLSSQGT LADRQ
DGYVSSSESGSHHQFVTSSGAGFPLPQHDSSGTC HIDNSS EADVEAATDLFLCPFLGSTGPMY
LKGNVYGSDPFETYHTGCS PDPRTVLMDHYEPSYIKKKECYPCSHPSEESCERSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLD F SANPEPASVASSNSFMGTGFKALRRPHLDAYS
SFGQPSDCQPRAFY LKAHSSPD LSGSEEDGKERTDFQEENHICTFKQTLENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

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FIGURE 107

CAAAACTTTCGCTCGCGGAGAGCGCCAGCTTGACTTGAATGGAAGGAGCCCGAGCCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCCTTCGCCCTTGTGGGGCGCCGCTCGCGGCCCGGGCGCAGCAGGGAAGGGGAAGCTGTGGTCTGCC
CTGCTCCAAGAGGCGCCATGTGTGAAACCGGAGAGCCCTGGGTGGTCCCGTCCCTTATCCCTCTTTATATA
GAAACCTTCCAACCTGGGAAGCGCAGCGCGAGGCGAGGAGGGCTCATGGTGAGCAGGAGGCGCGCTGATCTGCAG
GCGCAGAGCTTCCGAGTTTACAGATTTTTACAGATACCAAATGGAAGGCGAGGAGGCGAGAACAGCCTGCTGCTGGT
TCCATCAGCCTTGGCGCCACAGGCGCATCTGACTCGGCACCCCTCGCAGGCAACATGGGCCAGAGCGCGGTGCTGTC
TGCTCTGTGCTGCTGCTCGCGCCACAGCTGCACCTGGGACCTGTGCTTGGCGGTGAGGCGCCAGGATTTGGCCGAA
GTGGCGGCGCAGCCTGAGCCCGCAGGAAGAACGAATTTGGCGAGGAGGAGCCGTGCTGGTACTGAGCCCTGAGG
AGCCCGGAGCCTGGCCGAGCGCGGTGAGCTGCGCCCGAGACTGTGCTCTTGGCGAGGGGCGCTGTGGATCTGAGCTGTG
GCGGTATGACCTCTGTGAGTGTCCCGGGGGACCTGCCTGAGCAGCACCACCACTTCTCTGCAGAACCAACAGC
TGGAAAGATCTACCTCTGAGAGCTCTCCGGCTGCACCGGCTGGAGACTGAACCTGCAAAACCAACCTCCGCTGA
CTTCCCGAGGGCTCCAGAGAAGGGTGTGAGCATCTGACCAACTCAATTAACCTGTACTTGGCCAAATAACAGC
TGACCTTGGCACCCCGCTTCTGCCAAACGCCCTGATCAGTGTGGACTTGTGTCGCAACTATCTCACCAGAATCT
ATGGGCTCACTTTGGCCAGAGGCCAAACTTGAGGTCTGTGTACTTGCACAAACAAGCTGGCAGAGCGCGGGC
TGCCGACAGACTGTTCAACCGCTCCAGCAACGCTCGAGGTCTCTATCCTGTCCAGCAACTTCTTGGCCAGCTGC
CCAAGCACTGCGCGCTGCCCTGTACAAGCTGCACCTCAAGAACCAAGCTGGAGAAGATCCCCCGGGGGCCT
GCACCTCATGACTCTGCACAACAGATCACAGGCATTGGCCGCAAGACTTTCGCAACCACTTCTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCACAGGTGCACGCGCAGCCCTTCCGCAAGCTGCGCCTGTCTGC
GCTCGCTGGACCTGTGCGGCAACCGCTGCACACGCTGCCACCTGGGCTGCTCGAAATGTCCATGTGCTGGAAG
TCAAGCGCAATGAGCTGGCTGCTTGGCAGAGGGGCGCTGGCGGCAATGGCTCAGCTCGGTGAGCTGTACTTCA
CCAGCAACCGCATGCGCAGCGAGCCCTGGGGCCCGGTGCTGGGTGGACCTCGCCATCTGCAGCTGTGGACA
TCGCGGGAATCAGCTCACAGAGATCCCGAGGGGCTCCCGAGTCACTTGAGTACCTGTACTTGCAGAACAA
AGATTAGTGGCGTGGCCGCAATGCCCTTCGACTCCAGCGCCCACTCAAGGGGATCTTTCTCAGGTTTAAACAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCCTTCGGAGGCTGAAGCACTTCGAGTCTTGGACATTGAAGGCAACT
TAGAGTTTGGTGACATTTCAAGGACCGTGGCGCTTGGGGAAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGG
AGGAAGAGGAAACAAGATAGTGACAAAGTGATGAGATGTGACTAGGATGATGGACGCGCGGACTCTTTTCTGC
AGCACACGCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGACACCCAGCTGCACATGAGGCA
TCCACATGACACGGGCTGACACAGCTCTATATCCCAACCCCTTCCACGCGGTGTCCACGGCCAGACACATGC
ACACACATCACACCTCAAACACCGAGCTCAGCCACACACAATACCTCCAAACCAACACAGTCTCTGTACAC
CCCCATACCGCTGCCACGCGCTCTGAATCATGAGGGAAAGGGTCTGCCCTTGCCTTGGCACAACAGGCAACCA
TTCCCTCCCTGCTGACATGTGTATGCGTATGCATACACACACACACATGCAAGTCACTGTGCGAA
CAGCCCTCCAAGCCTATGCCACAGACAGCTCTTGCCCGAGCCAGAAATCAGCCATAGCAGCTCGCGCTGTGCCCT
GTCCATCTGTCCGTCCGTTCCCTGGAGAAGACAAAGGGTATCCATGCTCTGTGGCCAGGTGCGTGCACCCCTCT
GGAACTCACAAAGCTGGCTTTTATCTCTTCCATCTCTATGGGGAAGGAGGCTTTCAGGACTGTGGCCCTGGCC
TGGCCACCCCTGCTCTCCAGGTGCTGGGCGAGTCACTCTGCTAAGAGTCCCTCCCTTGCACGCCCTGGCAGGACA
CAGGCACTTTTCCAATGGGCAAGCCAGTGGAGGAGGATGGGAGAGCCCTGGGTGGCTGTGGGGCCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGGCTGAGCAGGGAGGAAGGACCGACTGTCACTTGGAGAGACACTTT
GTTCTTCAGGCCCTGTGGGGAGGTTTCGGGTGCTTTATTTTATTTCTTTCTTGAAGAAAAAATGATAAAAAAT
CTCAAGCTGATTTTCTGTTATAGAAAACTAATAAAAGCAATTACCTATCCCTGCAAAAAA

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FIGURE 108

MEGEEAEQPAWFHQPWPRGASDSAPPAGTMAQSRVLLLLLLLLPPQLHLGPNLAVRAPGFGRS
GGHLSPEENEFAEEEEPVLSPEEPGPGPAAVSCPRDCACSQEGVVD CGGIDLREFFPGDLP
EHTNHLSQLNNQLEKIYPEELSRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSSRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSV DANVLTPIRSLEYLLHNS
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPRRVRTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSPQVHRDAFRKLRLRLSLDLSGNRLHTLPPGLPRNVHLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

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FIGURE 109

GGGAGGGGGCTCCGGGCGCCGGCGCAGCAGACCTGCTCCGGCCGGCGCCTCGCCGCTGTCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGCGAGGGGCTGGGGGTTTCTCTGAGACTCTCAGAGGGCGGCTCCCATCGGCGCCCAACACCC
CAACCTGTCTCTCGGCGGCAGCTGGCGCTGCGCCCCAGGACCGCTGCCAAAGATGATTTTTCTCTGGCGCTGGT
GCTGGTATCTCTGCTTCACTCGAGCGGCGCGCGAGTTTCAGCGGAGGTTGGCCAGGCAAAATAGTGTCACTGAT
TGGCCTATGTTCGTTATGGTGGGAGGATTGACTGCTGCTGGGGCTGGGCTCGCCAGTCTTGGGGACAGTGTCAACC
TGTGTGCCAAACAGATGCAAACTAGTGAATGTATCGGGCCAAACAAGTGCAGATGTATCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCCTGAAGCCCCGGCCCTGTAAGGCACAGGTGCAATGAACACTTA
CGGACGCTACAAGTGCTACTGTCTCAACGGATATATGCTCATGCCGGATGGTTCTCTGCTCAAGTGCCCTGACCTG
CTCATGGCAAACTGTGAGTGGCTGTGATGTTGTTAAAGGACAAATACGGTGCAGTGCCCATCCCTGGGCT
GCACCTGGCTCTCAATGAGGAGGACCTGTGTAGTGTGTGATGAATGTGCTACAGGAAGAGCCTCTGGCCCTAGATT
TAGGCAATGTGTCAACACTTTTGGGAGCTACATCTCAAGTGTATAAAGGCTTCGATCTCATGTATATTGGAGG
CAAAATATCAATGTCACTGACATAGACGAATGCTCACTTGGTCAGTATCAGTGCAGCAGCTTGTCTGATGTTATATA
CGTACGTGGTCTCTACAAGTGCAAAATGTAAGAAGGATACAGGGGTGATGGACTGACTTGTGTATATATCCAAA
AGTTATGATTGAACCTTCAGGTCCAATTCATGTACCAAAGGAAATGGTACCATTTTAAAGGTTGACACAGGAAA
CAGGCCTACTCTAAGCCAAACAAGACCTACACCAAAGCAACACCAATTCCTACTCCACCACCACCACCACC
CCTGCACACAGAGCTCAGAAACCTCTACCACTCAACCCCAAGAGGCCAACCCCGGACTGACAACTATAGC
ACGAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAAACGGGTACAGACAGCCCTCAGAAACCAGAGG
AGATGTGTTTCAGTGTCTTGGTACACAGTTGTAATTTTGACCATGGACTTGTGATGGATCAGGAGAGAAGACAA
TGACTTGCACTGGGAACCAATCAGGAGCCACAGCAGGTGGACAATATCTGACAGTGTCCGACAGCCAAAGCCCCAG
GGGAAAAGCTGACAGCTTGGTCTACCTCTCGGCCCTCATGCATTCAGGAGACTGTGCTCTCAITTCAGGCA
CAAGGTGACCGGCTGCACTCTGCCACACTCCAGGTGTTTGTGAGAAAACACGGTGCCACAGGAGCAGCCCTGTG
GGGAGAAGATGGTGGCCACTGGCTGGAGGCAACACAGATCACTTGCAGGGGCTGCACTCAAGAGCGGAATCA
AAGATGAATTAAGGGTTGGAAAAAAGATCTATGATGGAAAAATTAAGGAATCGGGATTATGGACCTGGAGAG
AGAAGACTGAGGGGCAACCAATGATGGTTTCAAGTATATGAAGGGTTGGACAGAGAGGTTGGCGACCAAGCTG
TCTCCATATCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTAAAGGAGCAATTTCTTGGCAGG
GGCCATTGTTAGAACTCTCATAAAAAAAGAGTGTGAAAAATCTCAGTATCTCTCTCTCTTTCTAAAAAATTAGA
TAAAAAATTTGTCTATTTAAGATGGTTAAAGATGTTCTTACCAGGAAAGTAACAAATATAGAATTTCCCAAA
AGATGTTTGTATCTACTAGTAGTATGCAGTGAAAAATCTTTAGAACTAAATAATTTGGACAAGGCTTAATTTAGG
CATTTCCCTCTGACCTCCTAATGGAGAGGGATTGAAAGGGGAAGAGCCCAAAATGCTGAGCTCACTGAAATA
TCTCTCCCTTATGGCAATCTAGCAGTATTAAGAAAAAGGAAACTATTATTCCAAATGAGAGTATGATGGAC
AGATATTTTAGTATCTCAGTAATGTCTTAGTGTGGCGGTGGTTTCAATGTTTCTCATGGTAAAGGTAAGAACC
TTTCATTTGTTCAATGGATGATGTTTCAGATTTTTTTTTTTTAAAGAGATCCTTCAAGGAACACAGTTCAAGAG
ATTTTCATCGGGTGCACTCTCTCTGCTTCGTGTGTGACAAGTTATCTTGGCTGTGAGAAAGAGTGGCCTGCC
ACACCGGCAGACCTTCTCTCACTCATCAGTATGATTGATTTCTCTTATCAATGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGTGAACAATAGGTACAATAGAAGTCTTCTGTCAITTAACCTGGTAAAGGCAAGGCTGG
AGGGGGAATAAATCATTAAGCCTTTGAGTAACGGCAGAATATATGGCTGTAGATCCATTTTAAATGGTTCAAT
TCTTTATGGTCATATAACTGACAGCTGAAGATGAAGGGGAAAAATAAATGAAAAATTTACTTTTTCGATGCCAA
TGATACATTTGCACTAAAGTATGGAAGAGTTATCCAAAGTACTGTATAACATCTGTGTTATTTATTTATGTTT
CTAAAAATAAAAAATGTTAGTGGTTTTTCAATGGCCTAATAAAAAATTTATTTGTAATAAAAAACATCTGTTAGT

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FIGURE 110

MDFLALVLVSSSLYLQAAAEFDGRWPRQIVSSIGLCRYGGRIDCCGWARQSWGQCQPVCQP
RCKHGECIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDDVVKQIRCCQCPSPGLHLAPDGRTCVDVDECATGRASCPRFRQC
VNTFGSYICKCHKGFDLMYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHVPKNGTILKGDGTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPLPTELRTPLPPTTPTTGLTTIAPAASTPPGGITVDN
RVQTDPOKPRGDFVSVLVHSCNFDHGLCGWIREKDNLDLHWEPIRDPAGGOYLTVSAAKAPGG
KAARLVPLGLRLMHSGLCLSFRRHKVTGLHSGTLQVFVRKHGAHGAALWGRNNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

0902615-071001

FIGURE 111

CTTCTTTGAAAAGGATTATCACCTGATCAGGTTCTCTCTGCATTTGCCCCCTTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTTCTCTTCTTTGCAACAGGTGCTTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAGGCCCTCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTTGAGAGACCCCA
CACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTTCTGTACTTGGAAATACC
AACACAAGTTTCAACATGATGCCACCCAAATGCATCTGTGCTTATCAACCCACTGCGAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAGGGAATGGAATCTATCTGCCAGTCA
GAAGATACAAGTCACGGTTGATGATCCTGTCAAAAGCCAGTGGTGCAGATTATCCTCTCCCT
CTGGGGCTGTGGAGTATGTGGGGAACATGACCCTGACATGCCATGTGGAAGGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTTC
TCCCCAAAACAATACCTTTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCCTGGTGAGGAACCTGTCTAGTGAATGGAAGTGATATCATTATGCCCATCATATATTAT
GGACCTTATGGACTTCAAGTGAATTCGTATAAGGGCTAAAAGTAGGGGAAGTGTTTACTGT
TGACCTTGGAGAGGCCATCCTATTTGATTGTTCTGTCTGATTCTCATCCCCCAACACCTACT
CTGGATTAGGAGGACTGACAATACTACATATATCATTAAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCAGAAGACAATGGACTATGTGTGCTGTGCTTACAACAACATAAC
CGGCAGGCAAGATGAAACTCATTTCACAGTTATCATCACTTCGTTAGGACTGGAGAAGCTTG
CACAGAAAGGAAAATCATTGTCACTTTAGCAAGTATAACTGGAATATCACTATTTTGTATT
ATATCCATGTGTCTTCTCTTCTATGGAAAAAATATCAACCCATAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATTTTCAGGCCATGAAGATG
CTCTGGATGACTTCGGAATATATGAATTTGTTGCTTTTCCAGATGTTTCTGGTGTTCAGG
ATTTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATCGGGCAAGATTTGACAGTACAGT
GTATGAAGTTATTCAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGTGAACCTTTCATGG
GCTAAACAGTACATTCGAGTGAATTTCTGAAGAAACATTTTAAGGAAAAACAGTGGAAAAAGT
ATATTAATCTGGAATCAGTGAAGAAACAGGACCACACCTCTTACTCATTATTCTCTTTACA
TGCAGAAATAGAGGCATTTATGCAAAATGAACTGCAGGTTTTTCAGCATATACACAATGTCTT
GTGCAACAGAAAAACATGTTGGGGAATATTCCTCAGTGGAGAGTCGTTCTCATGCTGACGG
GGAGAACGAAAGTGACAGGGGTTTCTCTATAAGTTTGTATGAAATATCTCTACAAACCTCA
ATTAGTCTACTCTACATTTCACTATCATCAACACTGAGACTATCCTGTCTCACCTACAAA
TGTGGAACCTTACATTGTTGATTTTTCAGCAGACTTGTGTTTATTAATTTTTATTAGTG
TTAAGAAATGCTAAATTTATGTTTCAATTTTATTTCCAAATTTCTATCTTGTATTGTTACAA
CAAAGTAATAAGGATGGTTGTACAAAAACAAAACACTATGCCTTCTCTTTTTTTTCAATCACC
AGTAGTATTTTTGAGAAGACTTGTGAACACTTAAGGAAATGACATTTAAAGTCTTTATTTT
TTTTTTTCAAGGAAAGATGATTCAAATAAATTATTTCTGTTTTTGCTTTTAAAAA

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FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQNGTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHVEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMSDIIMPIIYYGPYGLQVNSDKGLKVGVEFTV
DLGEAILFDCSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTM DYVCCAYNNIT
GRQDETHFTVIIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRVSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

100170-5192060

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTTGCACTTCCCTGGCAGTCTGGTGTCTGT
GCTTTGGGGTCTCCCTGGACGCACGGGCGGCGGAGCAACGTTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTGCCCTGCT
TGTCAAAATCTTCAACCGGAATGGGAAAGTTTGTCTGAATGGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTACAGAGCAGCCAGGACTGAGTGGACGGTTTATCATAACTGCTC
TTCTACTATTATCATTGTAAAGATGGTGAATTTAGGCGCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAATCTTATAAGTGATAAAGAGTGGAAAGATATTGAGCCCGTTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAAATCTTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTTAGCAACTCTGTTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCTTTGTCTTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTTCAAAAAAT
TATTATCAGAATCTGCACAACCTTTGAAAAAAGTGGAGGAGGAACAAGAGCGGATGAAGAA
GATGTTTCAGAAGAAGAGCTGAAAGTAAAGAAGGAACAACAAGACTTCCACAGAATGC
CATAAGACAACGCTCTCTGGTCCATCATTTGGCCACAGATAAATCTTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTTGATAAAACAGAAGATTGATCATTTTGTTTGGTTTGAAGTG
AACTGTGACTTTTTTGAATATTGCAGGGTTCAGTCTAGATTGTCAATAATTTGAAGAGCTA
CATTTCAGAACATAAAAGCACTAGGTATACAAGTTTGAAATATGATTTAAGCACAGTATGATG
GTTTAAATAGTTCTCTAAATTTTGA AAAAATCGTGCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTTCAGTCTGAGTTTGA AAAATTACATTTCCCAAGTATTGCATTAT
TGAGGTATTTAAGAAGATTATTTTAGAGAAAAATATTCTCATTTGATATAATTTTCTCTG
TTTCACTGTGTGAAAAAAGAGATATTTCCATAAATGGGAAGTTTGCCCATTTGCTCTCAAG
AAATGTGTATTTCAAGTGACAAATTTCTGTTGCTTTTAGAGGTATATTCCAAAATTTCTTGT
ATTTTTAGGTTATGCAACTAATAAACTACCTTACATTAATTAATTACAGTTTTCTACACA
TGGTAATACAGGATATGCTACTGATTTAGGAAGTTTTTAAGTTCAATGGTATTCTCTGATTC
CAACAAAGTTGATTTTCTCTGTATTTTCTTACTTACTATGGGTACATTTTATTTT
CAAAATGGATGATAATTTCTTGGAACATTTTTATGTTTGTAGTAAACAGTATTTTGT
GTTTCAAACTGAAGTTTACTGAGAGATCCATAAATTGAACAATCTGTTGTAATTTAAAT
TTGGCCACTTTTTTCAGATTTTACATCATTTCTGCTGAACTTCAACTGAAAATGTTTTTT
TTTCTTTTGGATGTGAAGGTGAACATTTCTGATTTTGTCTGATGTGAAAAAGCCTTGGTA
TTTTACATTTTGA AAAATCAAGAAGCTTAATATAAAAGTTTGCAATTTCTACTCAGGAAAAAG
CATCTCTTGTATATGCTTAAATGTATTTTGTCTCATATACAGAAAGTCTTAATTGAT
TTTACAGTCGTAAATGCTTGATGTTTTAAATAATAACATTTTATATTTTTTAAAGACAA
ACTTCATATTATCTGTGTTCTTTCTGACTGGTAATATTGTGTGGGATTTCACAGGTAAAA
GTCAGTAGGATGGAAACATTTTAGTGATTTTACTCTTAAAGAGCTAGAAATACATAGTTTT
CACCTTAAAGAAAGGGGAAAAATCATAAATACAATGAATCACTGACCAATTAAGTAGAC
AATTTCTGTAATGTCCTCTCTTTCTAGGCTCTGTTGCTGTGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTTTCTTTAAAGCCCTCTCTTTAGAAATTTAAATATTTGATACATT
AAAGAGTTTGGATGTGTAACTTGTGATGCTTAGAAAAATATCCTAAGCACAAAATAACCT
TTCTAACCCTTCATTAAGCTGAAAAA AAAAAAAAAA

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FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMI EFYAPWCPACQNL
QPEWESFAEWGEDLEVNI AKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEFPVSSWFGPGSVLMSSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQYPYPYPSKLLSESAQPLKKVEEEQEAEDEEDVSE
EEAESKEGTNKDFPQNAIRQ RSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

0902515-011001

FIGURE 115

GCGAGTGTCCAGCTGCGGAGACCCGTGATAATTTCGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCAGTGGGACAGGCGGATTTGGAAGAGCGGG
AAGGTCCTGGCCCCAGAGCAGTGTGACACTTCCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCCCTGGTTTGGTGTCTGTGAGCTGTGTGCAGGCCGAATTCTTCACCTGTATTG
GGCACATGACTGACCTGATTATATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTTGTGGAGGAAGCCCAAGCTTTCCAAGATTAAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAAACACAGACTGGCCTGCGCTGGAGGACCTTGTCTCTGAGGACTCAGCTGCA
GGTTTTATCGCCCAACCTCTCTGTGCAGCGGCAGTTCTTCCCACTGATGAGGACGAGATAGG
AGCTGCCAAAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTTCCA
GAGGGGAACCTTCCAGGAACCAAGTACCAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCCTACAATGAAGGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCACAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGTCTTCAGTTGGGTGATCTGCACCGTGCCCTGGAGCTCACCCGCCGCTGCTC
TCCCTTGACCCCAAGCCACGAACGAGCTGGAGGGGAATCTGCGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAAGCTGAGCTAGCAACCCAGAAAGGCA
TCTATGAGAGGCCCTGTGGACTACCTGCCTGAGAGGGATGTTTACGAGAGCCTCTGTCTGGG
GAGGTGTCAAACCTGACACCCCGTAGACAGAAGAGGCTTTTCTGTAGGTACCACCATGGCAA
CAGGGCCCCACAGCTGCTCATTGCCCCCTTCAAAGAGGAGGACGAGTGGGACAGCCCGCACA
TCGTCAAGTACTACGATGTCTGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTTGCACGAGCCACCGTTTCGTGATCCCAAGACAGGAGTCTCACTGTGCCAGCTA
CCGGGTTTCCAAAAGCTCTTGGCTAGAGGAAGATGATGACCCTGTTGTGGCCCCAGTAAATC
GTCGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAAT
TATGGAGTGGGAGCAGTATGAACCGCACTTCGACTTCTCTAGGCGACCTTTTGCAGCGG
CCTCAAAACAGAGGGGAATAGGTTAGCGACGTTTCTTAACTACATGAGTGATGAGAAGCTG
GTGGTGCCACCGTCTTCCCTGATCTGGGGCTGCAATTTGGCCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTTGCGGAGCGGGGAAGGTGACTACCGAACAAGCATGCTGCCTGCCC
TGTGCTTGTGGGCTGCAAGTGGGTCTCCAATAAGTGGTTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAAGTTGACTTGACATCCTTTTCTGTCTTCCCTTCTGGTC
CTTCAGCCCCATGTCAACGTGACAGACACCTTTGTATGTTCCCTTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTTGTCTGGAGCAGAGGGAGACCATATAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTCAAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTTCAGTGAACCAAGTTCTGATACCTTGTTTTACATGTTTGTTTTAT
GGCATTCTATCTATTGTGGCTTTACCAAAAAATAAAATGTCCCTACCAGAAAAA

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FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALDELVLQDSAAGFIANLSVQRQFFP
TDEDEIGAALKMRLQDTYRLDPGTISRGEPLGPKYQAMLSVDDCFGMGRSAYNEGDIYYHTV
LWMEQVLKQLDAGEEATTTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEREKTLTNQTEAELATPEGIYERPDYLPERDVYESLCRGEQVKTLPKRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYVDVMSDEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHFDPS
RRPFDGLKTEGNRLATFLNYSMDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEQDYR
TRHAACPVLVGCWKVSNKWFHERGQEFRLPCGSTVEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

00902615-010001
100120-51920660

FIGURE 117

GCAGTATTGAGTTTACTTCTCCTCTTTTAGTGGAAGACAGACCATAATCCCAGTGTGAGTGAATGATTGT
TTCAITTTATTACCGTTTGGCTGGGGGTAGTTCGACACCTTACAGITGGAAGAGCAGGCAGAGGAGTGTGA
AGACAGGACAACTCTCTGGGGATGCTGGTCTGGGAAGCCAGCGGGCTTGTCTCTGTCTTTGGCTCATTGACCC
CAGGTTCTCTGGTTAAACCTGAAGCCTACTACTGGCCTGGTGGCCCAATTCATGTATCCTTGAGGCTGTGGCC
CTTGGGGCAACCACCTGCGACGGGCTTACCACCATGCGACTGAGCTCCCTGTGGCTCTGCTCGCGGCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGGTGAGCCTGAGCCTCTCGCGGTTTCTGGATCCAGGGGGAGGGAGAG
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGCGAGAGCTCGCTAGACCAAGTG
ATGAGACTCTCAAACCCGGATGTCCCTACTACAGGGACCCCAACAGCCCTACAGAAGGTGCTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGTCTGACTCCCGAGCTACACTGTCCA
CTTTGGCCGTGCTGTGAACCGTACGGTGGCCCACTCACTTCCCTCGGTTACTCTACTTCACTGGGACGGCGTCC
CCCGGCTCCAGCAGGGATGCAAGTGGTGTCTCATGGGATGAGCGGCCCTGGCTCATGTGAGAGACCTGTC
GCCACCTTCACACACACTTTGGGGCCGACTACGACTGGTTCTTCATCATGCGAGGATGACACATATGTGACGGCC
CCGCTGTGGCAGCCCTTGTCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGGCAGAGGAGTTTATTG
GGCCAGCTGATGAGTGGTCCGAGGAGACATTTCTAGTGCCTGCTGACAGAGTGGCTTGGACGCTGCCTCATGT
ACTCTCTGGGCGTGGCTGTGTCTCACAGCACAGGGGCAGCAGTATCGCTCATTTGAACGGCCAAAATAGGG
ACCCTGAGAAGGAAGGAGCTCGGCTTTCTGAGTGCCTTCCGCGTGACCCCTGTCTCCGAAGGTACCTCTCATGT
ACCGGCTCCAACACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATGAACAACCTGACGGCTCAGA
TCCGGAACCTGACGCTGTGACCCCGAAGGGGAGGCGAGGCTGAGCTGGCCGTTTGGCTCCCTGCTCCTTTTCA
CACACACTCTCGCTTTGAGGTGTGGGCTGGGACTACTTCACAGAGCAGCACACTTCTCTGTGAGATGGGG
CTCCCAAGTGCCCACTACAGGGGGCTAGCAGGGCGGACGTGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCGCTGCGCTTCCAGAAGCAGCGACTGCTCAACGGCTATCGCGCTTCGACCCAGCAC
GGGCATGGAGTACACCTTGGACCTGCTGTTGGAATGTGTGACACAGCGTGGGCACCGCGGGGCCCTGGCTCGCA
GGGTGAGCTGTGCGGCCACTGAGCCGGGTGGAATCTACCTATGCCCTATGTCACTGAGGCCACCCAGTGTG
AGCTGTGCTGCCACTCTGTGGCTGAAGCTGTGACGCCCGGCTTTCTCGAGGCGTTTTCAGCCCAATGTCC
TGGAGCCACGAGAACATGCACTTGTCACTGCTGCTGAGCGGCAAGAGAGGTGGCCGTGGAGCTCCAG
ACCAATTTCTTGGGTGAAGGCTGACGAGCGGAGTTAGAGCGACGGTACCCTGGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGCCCTTCCCAGGTGCGACTCATGAGCTGGTCTCGAAGAAGCACCTGTGGACACTCTCT
TCTTCTTACACCGGTGTGGACAAGGCTTGGGCCGAAGTCTCAACCGCTGTGCGCATGAATGCCATCTCTGGCT
GGCAGGCTCTTTTCCAGTCCATTTCCAGGAGTTCAATCTGCGCTGTCAACACAGAGATCACCCCAAGGGCCC
CGGGGCTGGCCCTGACCCCCCTCCCCCTCTGGTGCTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTG
ACCGGCAAGCTTCTGCGAGGGCTGCTTCTACAACGCTGACTACTGGGGGCGGAGCCCGCTGGCAGGTGAAC
TGGCAGGCGAGGAAGGAGGAAGCCCTGGAGGGGCTGGAGGTGATGGATGTTTCTCCGCTTCTCAGGGCTCC
ACCTCTTTTGGGGCGTAGAGCCAGGGCTGGTGAGAAAGTTCTCCCTGCGAGACTGACGCCCAAGCTCAGTGAAG
AACTCTACCAACGCTGCGCCTCAGCAACCTGGAGGGGCTAGGGGGCGGTGCCAGCTGGCTATGGCTCTCTTTG
AGCAGGAGCAGGCCAATAGCACTTAGCCCGCTGGGGCCCTAACCTCATTACCTTTTCTTTGTCTGCTCAGCC
CCAGGAAGGGCAAGTAGGTGGACAGATAGAGAATGTTGCTGTATTTTAAATATGAAATGTTATTAAT
ACATGTCTCTGCGC

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FIGURE 118

MRLSSLLALLRPALPLIILGLSLGCSLSLLRVSWIQEGEGDFPCVEAVGERGGPQNPDSSRARLD
 QSDDFKPRIVPYRRPNKPYKKVLRTRYIQTELGSRRERLLVAVLTSRATLSTLAVAVNRTV
 AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSSETLRHLHTHFGADYDWFIMQDDTY
 VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
 DILSARPDWEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
 GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPGEAGLSWVGLPAPFTPHSRFEV
 LGWDYFTEQHTFSCADGAPKCPLOGASRADVGDALETALEQLNRRYQPRLRFQKQRLNNGYR
 RFDPPARGMEYTLDDLLECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVLP
 VAEAAAAAPAFLEAFAANVLEPREHALLTLLLVYGPREGGRGAPDPFLGVKAAAEELERRYPG
 TRLAWLAVRAEAPSQVRLMDVVSKHPVDTLFFLT'VWTRPGPEVLNRCRMNAISGWQAFPP
 VHFQEFNPALSPQRSPPGPPGAGDPDPPSPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
 RARLAGELAGQEEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVKQFSLRDCSPRLSEELYHR
 CRLSNLEGLGGRAQLAMALFEQEQAQNST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
 399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
 558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

100170-572266

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCCGTGCGCGGCTGCGCTTTCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTTCTGAAAGCAGCTCCTTTTGAAGGGTGTGATGCTTGG
AAGCATTTTCTGTGCTTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCCTAACAAAGAAGATATCTTGAAATTTCA
GAGGATGAGCGCATGGAGCTCAGTAAGAGCTTTCGAGTATACTGTATTATCCTTGTAAACC
CAAAGATGTGAGTCTTTGGGCTGCAGTAAAGGAGACTTGGACCAAACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAATGTTAAAGTGTTCAGTCAATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCTTTGATAAGTATAGAGACCAATACAACTG
GTTCTTCTTGCACGCCCACTACGTTTGCTATCATTGAAAACCTAAAGTATTTTTGTAA
AAAAGGATCCATCACAGCCTTTCTATCTAGGCCACACTATAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAAACAGGGAGGGATGATTTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTTGCCTGAAATATGCTGGAGTATTGTCAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACCAATCTGTTGGGCTTTCTATTAAAGAGGCAATGACTTATCACC
CAACCAGGTAGTAGAAGGCTGTTGTTTCAGATATGGCTGTACTTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGATGTATGGGTATACCGCCTTAGGGCATTGGGCATATTTTCAAT
GATGCATTGGTTTTCTTACCTCCAAATGGTTCTGACAATGACTGAAGAAGTGGTAGAAAAGCG
TGAATATGATCTTTGTATAGGACGTGTGTTGTCATTATTGTAGTAGTAACACATATCCAA
TACAGCTGTATGTTTCTTTTCTTTTCTAATTTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTTAAATGAGGGTGGTTTTTTCTTTAAACACATGAACATTGTAATG
TGTTGGAAGAAGTGTTTTAAGAATAATAATTTGCAAATAAACTATTAAATAATATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTTTGTGATTGGTT
AAAAAATTTAACAGGTCCTTAGCGTTCTAAGATATGCAAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACTTTTAGCTGTGTGTTCCCTTTACTTCTAATACTGATTATGTTCT
AAGCCTCCCCAAGTTCCAATGGATTGCGCTTCTCAAATGTACAACCTAAGCACTAAAGAAA
ATTAAAGTGAAAGTTGAAAAAT

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FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHHHLQAPNKEDILKISEDERME
LSKSPRVYCIILVKPKDVSLLWAAVKETWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMGG
IVLSVESMKRLNSLLNIPEKCPEQGGMWIKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

09902645-071001

FIGURE 121

CCCACGCGTCCGATCTTACCAACAAAACACTCCTGAGGAGAAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAAACAAAAAACCAAAGAGAGAGAAAAAATGAATTCATCTAAATCAT
CTGAACACAAATGCACAGAGAGAGGATGCTTCTCTCCCAAATGTTCTTATGGACTGTTGCT
GGGATCCCATCCTATTTCTCAGTGCCGTGTTTCATCACCAGATGTGTGTGACATTTGCGCAT
CTTTCAAACCTGTGATGAGAAAAAGTTTCAGCTACCTGAGAAATTCACAGAGCTCTCTGCT
ACAATTATGGATCAGGTTCACTCAAGAATTGTTGTCCATTGAACTGGGAATATTTTCAATCC
AGCTGCTACTTCTTTTCTACTGACACCATTTCTGGGCGTTAAGTTTAAAGAAGTCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCTTTCTACAAGA
AACCTAAAATGAGAGAGTTTTTTATTGGACTGTCAGACCAGGTTGTCGAGGGTCAGTGCCAA
TGGGTGGACGGCACACCTTTGACAAAGTCTCTGAGCTTCTGGGATGTAGGGGAGCCCAACAA
CATAGCTACCTGGAGGACTGTGCCACCATGAGAGACTCTTCAAACCCAAGGC AAAATGGGA
ATGATGTAACTGTTTTCTCAATTATTTTCGGATTGTGAAATGGTAGGAATAAATCCTTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAAGGCACAACCTCAAATGTGTAAAGAAGGAAGAGCA
AGAACATGGCCACACCCACCGCCCCACACGAGAAATTTGTGCGCTGAACCTCAAAGGACTTC
ATAAGTATTTGTTACTCTGATACAAATAAAAAATAAGTAGTTTTAAATGTTAAAAAAAAAAAAA
AAA
AAAAA

0902615-071001

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSYNYGSGSVKNCCPLNWEYFQSSCYFFSTDTISWALS LKNC SAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQVVDGTPLTKSLSFWDVGEPNNIATLEDCATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

03602615-071004

FIGURE 123

GGGACTACAAGCCGCGCGCGCTGCCGCTGGCCCTCAGCAACCCCTCGA^{Atg}GGCGCTGAGGCGGCCACCCGCGAC
 TCCGGCTCTGCGCTCGGCTGCTGACTTCTTCCCTGCTGCTGCTTTTCAGGGGCTGCCTGATAGGGGCTGTAAATC
 TCAAAATCCAGCAATCGAAACCCAGTGGTACAGGAATTTGAAAGTGTGGAACCTGCTTTCATCATTTACGGATTCGCG
 AGACAAGTGACCCAGGATCGAGTGGAGGAAATTCAGATGAACAAACCATATGTGTTTTTTCAGACAAACAAA
 TTCAGGGAGACTTCCGCGGCTCGTGCAGAAATCTGGGGGAGACATCCCTGAAGATCTGGAATGTGACACGAGAG
 ACTCAGCCCTTTATCGCTGTGAGGTGCTGTGCTCGAAATGACCGCAAGGAAATTGATGAGATGTGATCGAGTTAA
 CTGTGCAAGTGAAGCCAGTGAACCCCTGCTGTAGAGTGCCGAGGCTGTACAGTAGGCAAGATGGCAACACTGC
 ACTGCGAGAGAGTGGAGGCCACCCCGGCTCACTCAGCTGGTATCGCAATGATGTACCATGTGCCACGGATT
 CCAGAGCCCAATCCAGATTTCGCAATTTCTTTTCCACTTAAACTCTGAAACAGGCATCTTGGTGTGTCACTGCTG
 TGCACAGGACGACTCTGGGCACTACTCTGATTCGTTCCAAATGACGAGGCTCAGCCAGGTGTGAGGAGCAGG
 AGATGGAAGTCACTGACCTGAACATTGGCGGAATTTTGGGGGGTTCTGCTGTGCTTACTGCTTACGCTGCTTAA
 TCACGTTGGGCATCTGCTGTGCATACAGACGTGGCTACTTCACTCAACAAATAACAGGATGGAGAAAGTTACAAGA
 ACCCAGGAAACCCAGATGGAGTTAACTACATCCCGCATGACGAGGAGGCGCATTCAGACACAACTCATCTGTTG
 TGATCTGAACCCGCGGTGTGGCTGAGAGCGCACAGAGCGCACCTGACATACCTCTGCTAGAAAATCCTGTCAA
 GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAGCTTTTCGTTTGGCCAAAGTTGACCA
 TCACTCTTCTTACTTAAACAGCCATGAATACAAGAAATTTTCTCAAGATGGACCCGGTAAATATAACACCAA
 GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGGTCTCTAATCTGTTTCTGGGCTGATTCGCGCATGAGTATAGG
 GTGATCTTAAAGAGTTTGTCTCACTGAACCGCCGCTGCGGCTGTGAAGCCAGCATGTTTCACTACTGTCGTT
 CAGACGACCCAGCACGACCATGTGAGATGGCGAGGTGGCTGGACAGCACCAGCAGCGCATCCCGCGGGGAAACCA
 GAAAGAGCTTCTTACACAGCAGCCTTACTTCTCGGCCACAGACACCCAGCAGTTCTTCTTAAAGGCTCTGC
 TGATCGGTGTGCGATGTCCATTGTGGAGAGCTTTTGGATCAGCATTTGTAAAAACAACAAATTCAGGAAG
 GTAAATTTGGTTGCTGGAGAGGGATCTTGCTGAGGAACCTGCTTGTCCAACAGGGTGTGAGGATTTAAGGAAA
 ACCTTCGCTCTAGGCTAAGCTGAATGGTACTGAAATATGCTTTCTATGGGTCTGTTTATTATATAAAATTT
 TACATCTAAATTTTGTCTAAGGATGATTTTGTATTATGAAAGAAATTTCTATTATAACTGTAAATATATTGT
 CATCAATGTTAAATAACCTATTTTAAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGTGTAAAT
 TGGAAATAATCAATAATTAAAGATATTTACCCAAGGAATCCTCTCATGGAGTTTACTGTGATGTTCTTTTCT
 CACACAAGTTTTAGCCTTTTTCACAGGGAACCTCATACTGTCTACATCAGACCATAGTTGCTTAGGAAAACCTT
 TAAAAATTTCCAGTTAAAGCATGTGAAATCAGTTTGCATCTCTTCAAAGAAACCTCTCAGGTAGCTTTGAAT
 GCCTCTTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAGCCCTCAGATGTACATACAGATG
 CCAGTCAGCTCTCTGGGTTGCGCAGGCGCCCCGCTCTAGCTCACTGTGCTGCTGCTGTCGACAGGAGGCCCT
 GCCATCTCTGGGCCCTGGCAGTGGCTGTGCCAGTGAAGCTTACTCACTGTCGCTTCTCATCCAGCACAGC
 TCTCAGGTGGGCACTGCAGGGAACCTGCTGTTCCATGTAGCTGCCAGCTTTGGGCTCTGCTGAACAGACCTCT
 TTTTGGTTATGAGTGGCTCAAAAATAGGGCCCCCAATGCTATTTTCTTTTAAAGTTTGTTTAATTTATTTGTT
 AAGATTGTCTAAGGCCAAAGGCAATTCGAAATCAAGTCTGTCAAGTACAATAACATTTTAAAAAGAAATGGAT
 CCCATGTTCTCTTTGCCACAGAGAAAGCACCCAGACGCCACAGGCTCTGTCGATTTCAAAACAAACATGAT
 GGAGTGGCGGCCAGTCCAGCCTTTTAAAGAACGTCAAGTGGAGCGACGAGGTGAAAGGCTGGCGGGGAGGAAG
 TGAACCGCTGAATCAAAGCAGTTTCTAAATTTGACTTTAAATTTTTCATCGCGCGAGGACACTGCTCCCATTT
 TGTGGGGGACATTAAACATCACTCAGAAGCTGTGTTCTCAAGAGCAGGTGTTCCAGCCTCACATGTCCTTGA
 GATGGCTCTCACTACTCACTTGTCTTTCAGCTTCCAGTGTCTTGGGTTTTTATATCTTGCACAGCTTTTGT
 AATTGCATACATGAGACTGTGTTGACTTTTTTAGTTATGTGAAACACTTTGGCGCAGGCGCCTGGCAGAGGCA
 GGAATGCTCTCAGCAGTGGCTCAGTGTCCCTGGTGTCTGCTGCAATGCACTCTGGAATCTCTACATGCAAGTTC
 CCTCCATCATTGCCACCTGTGTAGAGAGGGATGGCTCCCAACCTCAGGCTTGGGATTCACGCTCAGCCTCCT
 TCTTGGTGTCTATAGTATAGGATGGCTTATTGGCCCTCTCTTATACCTTAAACCTCTACATGATGCGCA
 TGGAAACAGGTTCTGAAAGATGAGAGAAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGATGCA
 CGGAAGGGAATACTCGTGATTTTAAAGATATGAATGTGACTCAAGCTCGAGGCCGATACGAGGCTGTGATTC
 GCCTTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTTGGCATTTTAAAC
 CTCATTTATAAAGCTTCAAAAAACCA

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FIGURE 124

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFFLLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQSTD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVPVCRVPAVPGKMATLHCQSESGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEYVDLNIIGGIIGG
VLVVLAVALITLGICCAIRRGYFINKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267

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